

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:08:13 ; Search time 23.82 Seconds

(without alignments)  
410.482 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MDAFVGTWKLVSSENFDDY.....KLVVECVMKGVSTRVYERA 132

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_1101.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	675	100.0	132	21	Human AFABP protei
2	625	92.6	132	21	Mouse AFABP protei
3	466	69.0	133	22	Mouse MDGI polypep
4	458	67.9	136	19	Human myelin P2 pr
5	453	67.1	131	12	MDGI active peptid
6	449	66.5	133	22	Human MDGI polypep
7	446	66.1	133	22	Bovine MDGI polypep
8	445	65.9	136	19	Bovine myelin P2 p
9	435.5	64.5	134	18	Porcine heart-fatt
10	399	59.1	132	18	Human cytoctatin I
11	399	59.1	132	19	Amino acid sequenc

12	399	59.1	132	19	AAW81106	Human cytoctatin I
13	399	59.1	132	20	AAW82403	Human 14-16 kDa FA
14	396	58.7	117	21	AAG03847	Human secreted pro
15	386.5	57.3	131	22	AAG66580	Human cytoctatin I
16	382	56.6	132	21	AAG03957	Human secreted pro
17	381	56.4	132	16	AAW75423	Mouse cellular x b
18	375	55.6	88	21	AAW58740	Breast and ovarian
19	366	54.2	135	15	AAW55866	Melanogenic inhibi
20	360	53.3	82	22	AAG75123	Human colon cancer
21	270	40.0	69	21	AAW65303	Human 5' EST relat
22	237	35.1	134	20	AAW68550	Human retinoid bin
23	229.5	34.0	133	16	AAW75643	Schistosoma mansoni
24	222	32.9	137	14	AAW42212	CRABP-I gene produ
25	210	31.1	56	21	AAW01405	Human secreted pro
26	201.5	29.9	138	14	AAW42211	CRABP-II gene prod
27	201.5	29.9	138	22	AAW76852	Human lung tumour
28	201.5	29.9	149	21	AAW58158	Lung cancer associ
29	194	28.7	99	21	AAW01603	Human secreted pro
30	186	27.6	160	21	AAW43403	Human cancer assoc
31	165	24.4	135	22	AAW38758	Human polypeptide
32	165	24.4	135	22	AAW60659	Human cellular ret
33	165	24.4	168	22	AAW40544	Human polypeptide
34	164	24.3	135	18	AAW30891	Human cytoctatin I
35	164	24.3	135	20	AAW32504	Human cytoctatin I
36	164	24.3	135	22	AAG66575	Human cytoctatin I
37	164	24.3	135	22	AAU02203	Retinol-binding pr
38	162	24.0	135	21	AAW92910	Human retinoid bin
39	136	20.1	156	22	AAU02202	Retinol-binding pr
40	122	18.1	107	18	AAW27561	Human cytoctatin I
41	122	18.1	107	18	AAW26581	Human cytoctatin I
42	122	18.1	107	20	AAW49535	Human cytoctatin I
43	122	18.1	107	20	AAW83929	Human growth inhib
44	115.5	17.1	106	22	AAG66579	Human cytoctatin I
45	110	16.3	55	9	AAW82557	Human cellular ret

## ALIGNMENTS

RESULT 1  
AAW90320  
ID AAW90320 standard; Protein; 132 AA.  
XX  
AC AAW90320;  
XX  
DT 22-NOV-2000 (first entry)  
XX  
DE Human AFABP protein sequence.  
XX  
KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;  
KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;  
KW serum cholesterol; therapy; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200047734-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-US03560.  
XX  
PR 12-FEB-1999; 99US-0119880.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Lee M, Perrella MA, Hotamisligil GS;  
XX  
DR WPI; 2000-506094/45.  
XX  
N-PSDB; AAA37717.  
XX  
Reducing expression of adipocyte fatty acid binding protein through  
PT administration of a compound is used to inhibit formation of an  
PT atherosclerotic lesion.

XX Disclosure; Page 14; 43pp; English.

XX This sequence represents the human AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.

XX Sequence 132 AA;

Query Match 100.0%; Score 675; DB 21; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-71;  
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYKKEVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
 Db 1 mcdafvgtwklvssefddymkevvgvatrkvagmakpnmliisvngdvitikssetfkn 60  
 Qy 61 TEISFILGOEFDEVTDADRKKVKTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
 Db 61 teisfilgofdevtdadrkvvkstltldggvlvnhvqvkgdgksttikrreddklvvevcvm 120  
 Qy 121 KGVTSRYVERA 132  
 Db 121 kgvtstryvera 132

RESULT 2  
 AAY90319  
 ID AAY90319 standard; Protein: 132 AA.

AC AAY90319;  
 XX 22-NOV-2000 (first entry)  
 DT Mouse AFABP protein sequence.  
 DE AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;  
 KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;  
 KW serum cholesterol; therapy; mouse.

XX Mus sp.  
 OS WO200047734-A1.  
 PN 17-AUG-2000.  
 PD 11-FEB-2000; 2000WO-US03560.  
 PF 12-FEB-1999; 99US-0119880.  
 PR (HARD ) HARVARD COLLEGE.  
 XX Lee M, Perrella MA, Hotamisligil GS;  
 XX WPI; 2000-506094/45.  
 DR N-PSDB: AAA37716.

XX Reducing expression of adipocyte fatty acid binding protein through  
 PT administration of a compound is used to inhibit formation of an  
 PT atherosclerotic lesion -

XX Disclosure; Page 14; 43pp; English.

XX This sequence represents the mouse AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.

XX Sequence 132 AA;

Query Match 92.6%; Score 625; DB 21; Length 132;  
 Best Local Similarity 91.7%; Pred. No. 2.9e-65;  
 Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYKKEVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
 Db 1 mcdafvgtwklvssefddymkevvgvatrkvagmakpnmliisvngdlvtirsetfkn 60  
 Qy 61 TEISFILGOEFDEVTDADRKKVKTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
 Db 61 teisfilgofdevtdadrkvvkstltldggvlvnhvqvkgdgksttikrreddklvvevcvm 120  
 Qy 121 KGVTSRYVERA 132  
 Db 121 kgvtstryvera 132

RESULT 3  
 AAG66576  
 ID AAG66576 standard; Protein: 133 AA.

AC AAG66576;  
 XX 22-OCT-2001 (first entry)  
 DT Mouse MDGI polypeptide.  
 DE Mouse; cytoostatin III; cytoostatic; epithelial cell growth;  
 KW milk production; breast involution; cardiac myocyte hypertrophy;  
 KW leukaemia; MDGI; mammary-derived growth inhibitor.

XX Mus sp.  
 OS US6232291-B1.  
 PN 15-MAY-2001.  
 PD 10-MAY-1999; 99US-0307817.  
 PF 19-MAR-1996; 96US-0013655.  
 PR 19-MAR-1997; 97US-0820825.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ni J, Yu G, Gentz R, Dillon PJ;  
 XX WPI; 2001-342775/36.

XX Cytostatin III polypeptides that modulate growth of epithelial cells,  
 PT stimulate milk production in humans and cows and promote involution of  
 PT breast, for research, biological, clinical and therapeutic purposes -

The invention relates to an isolated Cytostatin III polypeptide comprising a sequence selected from amino acids 1-135, 2-135, 108-135, 129-135 and 118-125, of a sequence of 135 amino acids fully defined in the specification. The polypeptide is useful for modulating growth of epithelial cells, for stimulating milk production in humans and cows, and for promoting involution of breasts. It is also useful for treating cardiac myocyte hypertrophy and leukaemia, and is useful for research, clinical and biological purposes. The present sequence is provided in the specification for comparison studies with human cytoastatin III.

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Query Match      69.0%; Score 466; DB 22; Length 133;
Best Local Similarity 67.9%; Pred.No.1.le-46;
Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY   1  MCDAFVGTKLVLSSENFDYMKVCGVGFATRKVAGCAKPNMIIISVNGDVITIKSESTKEN 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1  madafvvgcklvdsknfdydkmslgvfatrgvasmtkpttilekngdtitktgstfkn 60

QY   61 TEISFIILGOEPEYTDADRKKVKSIITLDGGVLVHVHQKDGSKTITKRREDDKLAVVEVCVM 120
      ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    61 teinfqlgiefdevtadrkvskvltidggklhvqkwnggettltrelvdgklltitlh 120

QY   121 KGVTSSTRVYER 131
      | | | | | | |
Db    121 gsvvstrtyek 131
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RESULT	4
AAW40227	
ID	AAW40227 standard; Protein; 136 AA.
XX	
AC	AAW40227;
XX	
DT	26-JUN-1998 (first entry)
XX	
DE	Human myelin P2 protein.
XX	
KW	Humam; myelin; P2 protein; treatment; inflammatory polyneuritis;
KW	Guillian-Barre syndrome; vasculitis; nerve inflammation;
KW	gammopathy.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 49
FT	/note= "encoded by AAT"
XX	
PN	WO9803647-A2.
XX	
PD	29-JAN-1998.
XX	
PF	18-JUL-1997; 97WO-DE01535.
XX	
PR	18-JUL-1996; 96DE-1029095.
XX	
PA	(GOLD/) GOLD R.
PA	(WEIS/) WEISHAUPT A.
XX	
PI	Gold R, Weishaupt A;
XX	
DR	WPI; 1998-120772/11.
N-PSDB; AAVI0405.	
XX	
PPT	Recombinant myelin proteins for treating T-cell mediated disease of
PPT	peripheral nervous system - by high dose antigen therapy, causing
PPT	apoptosis in T cells, for treating e.g. polyneuritis or

PT  
XX  
XX  
PS  
XX  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
XX  
SQ

Gullian-Barre syndrome  
Disclosure; Fig 4; 14pp; German.  
The present sequence is the human myelin P2 protein, which can be used to treat T-cell mediated diseases of the peripheral nervous system, especially chronic-inflammatory polyneuritis, Gullian-Barre syndrome, vasculitis and nerve inflammation in cases of gammopathy.  
Sequence 136 AA;

Query Match	67.9%;	Score 458;	DB 19;	Length 136;
Best Local Similarity	66.9%;	Pred. No. 1e-45;		
Matches 87;	Conservative 17;	Mismatches 26;	Indels 0;	Gaps
Qy	1	MCDAFVGTWKLVSSENFDYMKVGVGFATPKRVAGMAKPNKILSVNGDVLTIKSETFKN	60	
		1 :   :                                     :       :		
Db	1	msnflgcwklvsennfdymkaigvgatrkignakptvilskkgdilitrestfkn	60	
		1 :   :                                     :       :		
Qy	61	TEISFIILGQGFDEVTADDRVKVSTITITDGGVLVHVQKWDGKSTTIKRREDDKLWVECV	120	
		1 :   :                                     :       :		
Db	61	teisfklgqgfdeettadnrktsivtlgrqslngqvrdgkettikrklvngkmvaeckm	120	
		1 :   :                                     :       :		
Qy	121	KGVTSTRVYE	130	
		1 :		
Db	121	kgvvcctrlvd	130	
		1 :		

RESULT	5	
AAARI3559		
ID	AAARI3559	standard; protein; 131 AA.
XX	XX	
XX	AAARI3559;	
XX	XX	
DT	01-NOV-1991	(first entry)
XX	XX	
XX	MDGI	active peptides.
DE	XX	
XX	XX	Proliferation; inhibition; mammary-derived growth inhibitor.
KW	XX	
XX	XX	
OS	XX	Synthetic.
XX	XX	
Key	XX	Location/Qualifiers
Peptide	XX	69..78
FT	FT	/label= active_peptide
FT	FT	/note= "claim 10"
FT	FT	121..131
Peptide	XX	
FT	FT	/label= active_peptide
FT	FT	/note= "claim 11"
XX	XX	
XX	XX	DE4005062-A.
PN	XX	
XX	XX	22-AUG-1991.
XX	XX	
XX	XX	
PF	15-FEB-1990;	90DE-4005062.
XX	XX	
XX	15-FEB-1990;	90DE-4005062.
PR	XX	
XX	XX	(GROS/) GROSSE R.
PA	XX	
XX	XX	
Grosse R,	Langen P,	Bohmer FD, Wallukat G;
XX	XX	
PI	XX	WPI; 1991-253439/35.
DR	XX	
XX	XX	
XX	XX	Mammary-derived Growth Inhibitor peptide(s) - and antibodies
PT	PT	useful in biotechnology and medicine as proliferation inhibitors
PT	PT	e.g. of carcinoma cells
XX	XX	
XX	XX	Disclosure; Page 2; 6pp; German.
PS	XX	
XX	XX	
XX	XX	The indicated peptides and the peptides represented in AARI3560 and







CC adenocarcinoma, in particular, cancers of neurological origin such as  
 CC cancers of the breast and kidney. The products can also be used for  
 CC detection, diagnosis and drug screening.  
 XX  
 SQ Sequence 132 AA;

Query Match 59.1%; Score 399; DB 19; Length 132;  
 Best Local Similarity 56.8%; Pred. No. 7.6e-39;  
 Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGATRKVAGMAKPMNIISVNGDVITIKSESTFKN 60  
 Db 1 mveafcatwkltnsqnfdeymkalgvgfatrgvgnvtkptvilsqegdkvvtlsltfkn 60  
 QY 61 TEISFILGOEFDEVTDADRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVVECV 120  
 Db 61 teisfqlgeefdettdaddrncksvvslgdklvhikwdgktnfvreikdgkmvmtltf 120  
 QY 121 KGVSTRYVERA 132  
 Db 121 gdvavvrhyeka 132

RESULT 12  
 AAW81106  
 ID AAW81106 standard; Protein; 132 AA.  
 AC AAW81106;  
 DT 29-JAN-1999 (first entry)  
 DE Human cytostatin II.  
 KW Human; cytostatin; cell growth; tumour; nervous system;  
 KW viral infection; microbial infection.  
 OS Homo sapiens.  
 XX WO9844109-A1.  
 XX 08-OCT-1998.  
 XX 25-MAR-1998; 98WO-US05839.  
 XX 27-MAR-1997; 97US-0041645.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX (LONG-) LONG ISLAND JEWISH MEDICAL CENT.  
 XX Gentz RL, Nardelli B, Ni J, Shi YE, Yu G;  
 WPI: 1998-557110/47.  
 DR N-PSDB; AAV68225.  
 XX  
 PT New isolated human cytostatin II - used to develop products for the  
 PT treatment of e.g. cancers or viral or microbial infections or for  
 PT protecting nervous system cells from toxic agents  
 XX  
 PS Claim 1; Fig 1; 73pp; English.  
 CC The nucleotide sequence encoding Human cytostatin can inhibit cell growth  
 CC and modulate differentiation. The cytostatin II polypeptides can be used  
 CC for inhibiting tumour growth in a subject, for stimulating growth of or  
 CC protecting nervous system cells from toxic agents or for protecting  
 CC against or treating viral or microbial infections in mammals. The  
 CC products can also be used e.g. to modulate angiogenesis, to modulate  
 CC breast development and milk production. They can also be used in  
 CC cerebellar granular cells and photo receptor cells to provide protection  
 CC from lipid peroxidation associated with the oxidative stress induced  
 CC during early stages of ischemia, apoptosis, and excitatory amino acid  
 CC induced cell death. The retinoid binding potential of cytostatin II  
 CC may be used on photo receptor cells in vivo or in vitro. The activity of

CC haematopoiesis indicates a possible immunosuppressive activity or a  
 CC lineage specific stimulation of haematopoiesis which could be used for  
 CC treating conditions requiring immunosuppression. Antagonists to  
 CC cytosatin II may be used in vivo to induce deficiencies or enhancement  
 CC in the immune or in the haematopoietic systems. They may be used e.g. to  
 CC treat cardiac myocyte hypertrophy or leukemia.  
 XX  
 SQ Sequence 132 AA;

Query Match 59.1%; Score 399; DB 19; Length 132;  
 Best Local Similarity 56.8%; Pred. No. 7.6e-39;  
 Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGATRKVAGMAKPMNIISVNGDVITIKSESTFKN 60  
 Db 1 mveafcatwkltnsqnfdeymkalgvgfatrgvgnvtkptvilsqegdkvvtlsltfkn 60  
 QY 61 TEISFILGOEFDEVTDADRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVVECV 120  
 Db 61 teisfqlgeefdettdaddrncksvvslgdklvhikwdgktnfvreikdgkmvmtltf 120  
 QY 121 KGVSTRYVERA 132  
 Db 121 gdvavvrhyeka 132

RESULT 13  
 AAW82403  
 ID AAW82403 standard; Protein; 132 AA.  
 AC AAW82403;  
 DT 23-FEB-1999 (first entry)  
 DE Human 14-16 kDa FABP analogue GEN 128B10 protein.  
 KW FABP; detection; gene expression; analogue; GEN 128B10.  
 OS Homo sapiens.  
 XX JPL0286089-A.  
 XX 27-OCT-1998.  
 XX 15-APR-1997; 97JP-0096908.  
 XX 15-APR-1997; 97JP-0096908.  
 XX (SAKA) OTSUKA PHARM CO LTD.  
 XX WPI: 1999-063481/06.  
 DR N-PSDB; AAV73482, AAV73483.  
 XX  
 PT New human rab7GFP-combined analogous protein gene - useful for  
 PT detection of its expression in tissues  
 XX  
 PS Example 3; Page 24; 35pp; Japanese.  
 CC This sequence represents a novel human 14-16 kDa FABP protein analogue,  
 CC GEN 128B10. The gene is useful for the detection of gene expression in  
 CC various tissues.  
 XX  
 SQ Sequence 132 AA;

Query Match 59.1%; Score 399; DB 20; Length 132;  
 Best Local Similarity 56.8%; Pred. No. 7.6e-39;  
 Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGATRKVAGMAKPMNIISVNGDVITIKSESTFKN 60  
 Db 1 mveafcatwkltnsqnfdeymkalgvgfatrgvgnvtkptvilsqegdkvvtlsltfkn 60

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QY      61 TEISFILGQBFDEVTADDRKVKSTITLDGGVLVHVQKWGDGKSTTIKKREDDDLKVVECVM 120
        ||||| :||| :|||| | :||| ||| :||||| | :| :|||
Db      61 teisfqlgeeffettaddrcknksvvsldgklvhqkgdgketnfvreikdgmvmtltf 120
        ||||| :||| :|||| | :||| ||| :||||| | :| :|||

QY      121 KGYTSTRVIYERA 132
        | :| :||| :|
Db      121 gdvavviyehaka 132
        | :| :||| :|

RESULT 14
AAG03847
ID      AAG03847 standard; Protein; 117 AA.
XX
XX      AAG03847;
DT
DT      06-OCT-2000 (first entry)
XX
XX      Human secreted protein, SEQ ID NO: 7928.
XX
XX      Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW      gene therapy; chromosome mapping.
XX
XX      Homo sapiens.
OS
XX
XX      EP1033401-A2.
PN
XX
XX      06-SEP-2000.
PD
XX
XX      21-FEB-2000; 2000EP-0200610.
PF
XX
XX      26-FEB-1999; 99US-0122487.
PR
XX
XX      (GEST ) GENSET.
PA
PI      Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX      WPI; 2000-500381/45.
DR      N-PSDB; AAC03853.
XX
XX
XX      New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT      obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT      diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX      Claim 13; SEQ ID 7928; Tlpp + CD-ROM; English.
XX
XX      The present sequence is a polypeptide encoded by one of a large number
CC      of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC      were prepared from total human RNAs or polyA+ RNAs derived from 30
CC      different tissues. EST sequences usually correspond mainly to the 3'
CC      untranslated region (UTR) of the mRNA because they are often obtained
CC      from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC      isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC      those cases where longer cDNA sequences have been obtained, the full 5'
CC      UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC      ends and can therefore be used to obtain full length cDNAs and genomic
CC      DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC      chromosome mapping procedures. They are used to obtain upstream
CC      regulatory sequences and to design expression and secretion vectors.
XX
XX      Sequence 117 AA;

Query Match          58.7%; Score 396; DB 21; Length 117;
Best Local Similarity 69.1%; Pred. No. 1.4e-38;
Matches 76; Conservative 13; Mismatches 21; Indels 0; Gaps

QY      1 MCDAFVGTWKLVSSENDDYMKGVGVGFATRKVAGMAKNMIISVNGDVTTIKSESTFN 60
        | :| :||||| :||| :||| :||| :||| :||| :||| :|||
Db      1 msnkflgtwklvsennfdymkalgvglatrkignlakptvliskgditirtestfn 60
        | :| :||||| :||| :||| :||| :||| :||| :||| :|||

QY      61 TEISFILGQBFDEVTADDRKVKSTITLDGGVLVHVQKWGDGKSTTIKKRE 110
        ||||| :||| :|||| | :||| ||| :||||| | :| :|||

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[illegible]

RESULT 2  
US-08-470-298B-7  
Sequence 7, Application US/08470298B  
Patent No. 5844081  
GENERAL INFORMATION:  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: YU, GUO-LIANG  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: CYTOSTATIN I  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSES: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850

[illegible]

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RESULT      3
US-08-820-825-11
; Sequence 11, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-11

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	Query Match	69.0%;	Score 466;	DB 2;	Length 133;
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	Matches	89;	Conservative 15;	Mismatches 27;	Indels 0; Gaps
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Db	1	MADAFTGWLKVDKSNFDDYMKSLGVGFATRQVASTKPTTIEKNGDDTIIKTQSTFKN	60		
Qy	61	TEISFILGQEFDEVTAADRRKVKSTIIDGVLVHVQKWDGCKSTTKRKREDDKLVCEVCM	120		
Db	61	TEINFQLGIEFDEVTAADRRKVKSLVTLDDGKLLHVQKNGQETTLRELVDGKLLIITLTH	120		
Qy	121	KGVTSTRYER	131		
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RESULT      4
US-09-023-073A-7
; Sequence 7, Application US/09023073A
; Patent No. 5,977,309
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11

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[illegible]

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Db	61	TSFKLGQFEETADNR	KTKSVTL	QRLGSLNQV	QWQDKETT	IKRKLNVGR	KVAECKM	120
Qy	121	KGVTSTRVYER	131					
Db	121	KGVCSTRIVEK	131					

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RESULT 9
US-09-023-073A-11
: Sequence 11, Application US/09023073A
: Patent No. 5977309
: GENERAL INFORMATION:
: APPLICANT: Ni, Jian
: APPLICANT: Gentz, Reiner
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Rosen, Craig A
: TITLE OF INVENTION: Cytostatin I
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESS: HUMAN GENOME SCIENCES, INC.
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MARYLAND
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Versi
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/023-073A
: FILING DATE: 13-FEB-1998
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Wales, Michele M.
: REGISTRATION NUMBER: P-43,975
: REFERENCE/DOCKET NUMBER: PFI75D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 301-610-5772
: TELEFAX: 301-309-8439
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 132 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-023-073A-11

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Db 1 MSNKFLGTWKLIVSSSEFDDYMKALGVGLATRKLGNAKPTVIISKGGDIIRITESTEKN 60
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY* 61 TETSFILGQGFDEVTADRRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDKLVVECVN 120
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Db 61 TETSFILGQGFEEVTADRRKTSIVTLQKSLQVQRWDGKETTIIKRKLGVKMWAECKM 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 KGVTSRIVYER 131
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Db 121 KGVVCTRIVYK 131
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RESULT 10
US-09-361-737-11

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: Sequence 11, Application US/09361737
: Patent No. 6287812
: GENERAL INFORMATION:
:   APPLICANT: Ni, Jian
:   APPLICANT: Gentz, Reiner
:   APPLICANT: Yu, Guo-Liang
:   APPLICANT: Rosen, Craig A
:   TITLE OF INVENTION: Cytostatin I
:   NUMBER OF SEQUENCES: 11
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: HUMAN GENOME SCIENCES, INC.
:     STREET: 9410 KEY WEST AVENUE
:     CITY: ROCKVILLE
:     STATE: MARYLAND
:     COUNTRY: USA
:     ZIP: 20850
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: Patent In Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09361,737
:     FILING DATE:
:     CLASSIFICATION:
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: 09/023,073
:     FILING DATE: 13-FEB-1998
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Wales, Michele M.
:       REGISTRATION NUMBER: P-43,975
:       REFERENCE/DOCKET NUMBER: PF175D2
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: 301-610-5772
:       TELEFAX: 301-309-8439
:     INFORMATION FOR SEQ ID NO: 11:
:       SEQUENCE CHARACTERISTICS:
:         LENGTH: 132 amino acids
:         TYPE: amino acid
:         STRANDEDNESS: single
:         TOPOLOGY: linear
:       MOLECULE TYPE: protein
: US-09-361-737-11

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[illegible]

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RESULT 11
US-08-409-731A-10
; Sequence 10, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CYTOSTATIN I
; NUMBER OF SEQUENCES: 11

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CORRESPONDENCE ADDRESS:
ADDRESS: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-409-731A-10

Query Match 66.5%; Score 449:
Best Local Similarity 64.9%; Pred. No. 6:
Matches 85; Conservative 16; Mismatch
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QY 61 TEISILGGEFFEDVTADRRVKVSTITLDGGVLVHVQ
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DB 61 TEISFKLGVFEFDTTADRRVKVSIITLDGGKLVLHQ
QY 121 KGVTSRTVRYER 131
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DB 121 GTAVCTRTRYEK 131

RESULT 12
US-08-470-298B-10
Sequence 10, Application US/08470298B
Patent No. 5844081
GENERAL INFORMATION:
APPLICANT: NI, JTAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Versi

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: FABP (FIGURE 2)
US-08-470-298B-10

Query Match          66.58; Score 449; DB 2; Length 133;
Best Local Similarity 64.98; Pred. No. 6.3e-47;
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QY   121 KGVTSRTRYER 131
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Db   121 GTAVCTRTYEK 131

RESULT 13
US-08-820-825-13
; Sequence 13, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504

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Db 61 TEISFKLGVEFDETTADDRKVKSIVTLDGKLVHLQKWGDGQETTLVRELIDGKLLTLTH 120  
Qy 121 KGVISTRVYER 131  
|| ||:  
Db 121 GTAVCTRTYEX 131

Search completed: January 24, 2002, 09:15:40  
Job time: 382 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 09:14:28 ; Search time 97.19 Seconds  
(without alignments)  
377.104 Million cell updates/sec

Title: US-09-905-235-1  
Perfect score: 675  
Sequence: 1 MCDFAVGTWKLVSSENFDDY.....KLVVECMKGVSTRVYERA 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA\_Main.\*

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- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
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- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*
- 24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	132	17 US-09-391-053-1	Sequence 1, Appl1
2	675	100.0	132	17 US-09-391-053A-1	Sequence 1, Appl1
3	675	100.0	132	19 US-09-503-596-4	Sequence 4, Appl1
4	675	100.0	132	23 US-09-905-235-1	Sequence 1, Appl1
5	675	100.0	136	21 US-09-760-469-913	Sequence 913, App
6	675	100.0	136	21 US-09-760-469-915	Sequence 915, App
7	675	100.0	136	21 US-09-760-469-917	Sequence 917, App
8	675	100.0	136	21 US-09-760-469-1429	Sequence 1429, App
9	675	100.0	136	21 US-09-760-469-1432	Sequence 1432, App

10	675	100.0	136	21	US-09-760-469-1433	Sequence 1433, Ap
11	675	100.0	136	21	US-09-760-469-1434	Sequence 1434, Ap
12	649	96.1	129	22	US-09-834-366-17169	Sequence 17169, A
13	649	96.1	129	24	US-60-197-873-17169	Sequence 17169, A
14	625	92.6	132	19	US-09-503-596-5	Sequence 5, Appl1
15	572	84.7	132	20	US-09-699-146-172	Sequence 172, App
16	507	75.1	157	24	US-60-212-664-606	Sequence 606, App
17	488	72.3	97	16	US-09-216-665-18	Sequence 18, Appl
18	467	69.0	133	12	US-08-825-783-6	Sequence 6, Appl1
19	466	69.0	131	1	PCT-US96-03697-11	Sequence 11, Appl
20	466	69.0	131	14	US-09-023-073-7	Sequence 7, Appl1
21	466	69.0	133	1	PCT-US96-01640-7	Sequence 7, Appl1
22	466	69.0	133	8	US-08-470-298A-7	Sequence 7, Appl1
23	466	69.0	133	21	US-09-734-036-11	Sequence 11, Appl
24	463	68.6	132	1	PCT-US96-01640-11	Sequence 11, Appl
25	463	68.6	132	8	US-08-470-298A-11	Sequence 11, Appl
26	463	68.6	132	14	US-09-023-073-11	Sequence 11, Appl
27	463	68.6	138	22	US-09-834-366-15504	Sequence 15504, A
28	463	68.6	138	24	US-60-197-873-15504	Sequence 15504, A
29	463	68.6	141	21	US-09-760-469-903	Sequence 903, App
30	463	68.6	141	21	US-09-760-469-1419	Sequence 1419, App
31	449	66.5	133	1	PCT-US96-01640-10	Sequence 10, Appl
32	449	66.5	133	1	PCT-US96-03697-13	Sequence 13, Appl
33	449	66.5	133	8	US-08-470-298A-10	Sequence 10, Appl
34	449	66.5	133	12	US-08-825-783-7	Sequence 7, Appl1
35	449	66.5	133	14	US-09-023-073-10	Sequence 10, Appl
36	449	66.5	133	21	US-09-734-036-13	Sequence 13, Appl
37	449	66.5	133	23	US-09-948-941-307	Sequence 307, App
38	449	66.5	137	21	US-09-760-469-910	Sequence 910, App
39	449	66.5	137	23	US-09-948-941-358	Sequence 358, App
40	446	66.1	133	21	US-09-734-036-12	Sequence 12, Appl
41	437	64.7	138	20	US-09-699-146-173	Sequence 173, App
42	430.5	63.8	132	1	PCT-US96-03697-12	Sequence 12, Appl
43	428	63.4	141	21	US-09-758-471-3729	Sequence 3729, Ap
44	417	61.8	105	22	US-09-834-366-14769	Sequence 14769, A
45	417	61.8	105	24	US-60-197-873-14769	Sequence 14769, A

## ALIGNMENTS

RESULT 1  
US-09-391-053-1  
; Sequence 1, Application US/09391053  
; GENERAL INFORMATION:  
; APPLICANT: Robt, Jeffrey A.  
; APPLICANT: Biller, Scott A.  
; APPLICANT: Jacobson, Bruce L.  
; APPLICANT: Parker, Rex A.  
; APPLICANT: Jamil, Haris  
; APPLICANT: Kodukula, Krishna  
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR  
; TITLE OF INVENTION: AND COMBINATION  
; FILE REFERENCE: LA24aSequenceListing  
; CURRENT APPLICATION NUMBER: US/09/391,053  
; CURRENT FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: 60/100,677  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-391-053-1

Query Match 100.0%; Score 675; DB 17; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2,1e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
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Db 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
QY 121 KGVTSRTRYERA 132  
Db 121 KGVTSRTRYERA 132

RESULT 2  
US-09-391-053A-1  
; Sequence 1, Application US/09391053A  
; GENERAL INFORMATION:  
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY  
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND COM  
; FILE REFERENCE: LA24a  
; CURRENT APPLICATION NUMBER: US/09/391,053A  
; CURRENT FILING DATE: 1999-09-07  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-391-053A-1

Query Match 100.0%; Score 675; DB 17; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.1e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
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Db 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
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Db 121 KGVTSRTRYERA 132

RESULT 3  
US-09-503-596-4  
; Sequence 4, Application US/09503596  
; GENERAL INFORMATION:  
; APPLICANT: Lee et al.  
; TITLE OF INVENTION: Inhibiting formation of Artherosclerotic Lesions  
; FILE REFERENCE: 21509-042  
; CURRENT APPLICATION NUMBER: US/09/503,596  
; CURRENT FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 60/119,880  
; PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-503-596-4

Query Match 100.0%; Score 675; DB 19; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.1e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
Db 1 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60

QY 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
Db 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
QY 121 KGVTSRTRYERA 132  
Db 121 KGVTSRTRYERA 132

RESULT 4  
US-09-905-235-1  
; Sequence 1, Application US/09905235  
; GENERAL INFORMATION:  
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY  
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND CO  
; FILE REFERENCE: LA24a  
; CURRENT APPLICATION NUMBER: US/09/905,235  
; CURRENT FILING DATE: 2001-07-13  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-905-235-1

Query Match 100.0%; Score 675; DB 23; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.1e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
Db 1 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
QY 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
Db 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
QY 121 KGVTSRTRYERA 132  
Db 121 KGVTSRTRYERA 132

RESULT 5  
US-09-760-469-913  
; Sequence 913, Application US/09760469  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ54  
; CURRENT APPLICATION NUMBER: US/09/760,469  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1983  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 913  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-469-913

Query Match 100.0%; Score 675; DB 21; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.2e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
Db 5 MDAFVGTVKLVSSNFDDYMKVGVGATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 64  
QY 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120

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Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 124  
QY 121 KGVSTRVYERA 132  
|||||  
Db 125 KGVSTRVYERA 136  
|||||

RESULT 6  
US-09-760-469-915  
; Sequence 915, Application US/09760469  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT254  
; CURRENT APPLICATION NUMBER: US/09/760,469  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1983  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 915  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-469-915

Query Match 100.0%; Score 675; DB 21; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.2e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
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Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64  
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QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
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Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 124  
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QY 121 KGVSTRVYERA 132  
|||||  
Db 125 KGVSTRVYERA 136  
|||||

RESULT 7  
US-09-760-469-917  
; Sequence 917, Application US/09760469  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT254  
; CURRENT APPLICATION NUMBER: US/09/760,469  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1983  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 917  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-469-917

Query Match 100.0%; Score 675; DB 21; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.2e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
|||||  
Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64  
|||||  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
|||||

Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 124  
QY 121 KGVSTRVYERA 132  
|||||  
Db 125 KGVSTRVYERA 136  
|||||  
RESULT 8  
US-09-760-469-1429  
; Sequence 1429, Application US/09760469  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT254  
; CURRENT APPLICATION NUMBER: US/09/760,469  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1983  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1429  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-469-1429

Query Match 100.0%; Score 675; DB 21; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.2e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
|||||  
Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64  
|||||  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
|||||  
Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 124  
|||||  
QY 121 KGVSTRVYERA 132  
|||||  
Db 125 KGVSTRVYERA 136  
|||||

RESULT 9  
US-09-760-469-1432  
; Sequence 1432, Application US/09760469  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT254  
; CURRENT APPLICATION NUMBER: US/09/760,469  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1983  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1432  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-469-1432

Query Match 100.0%; Score 675; DB 21; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.2e-67;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
|||||  
Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64  
|||||  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120  
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Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 124  
|||||

QY 121 KGVSTRVYERA 132  
| | | | | | | | | |  
Db 125 KGVSTRVYERA 136

## RESULT 10

US-09-760-469-1433  
; Sequence 1433, Application US/09760469  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ54  
; CURRENT APPLICATION NUMBER: US/09/760,469  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1983  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1433  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-469-1433

Query Match 100.0%; Score 675; DB 21; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.2e-67; Indels 0; Gaps 0;  
Matches 132; Conservative 0; Mismatches 0;

QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
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Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEVCVM 120  
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Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEVCVM 124  
QY 121 KGVSTRVYERA 132  
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Db 125 KGVSTRVYERA 136

## RESULT 11

US-09-760-469-1434  
; Sequence 1434, Application US/09760469  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ54  
; CURRENT APPLICATION NUMBER: US/09/760,469  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1983  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1434  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-469-1434

Query Match 100.0%; Score 675; DB 21; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.2e-67; Indels 0; Gaps 0;  
Matches 132; Conservative 0; Mismatches 0;

QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
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Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEVCVM 120  
| | | | | | | | | |  
Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEVCVM 124

QY 121 KGVSTRVYERA 132  
| | | | | | | | | |  
Db 125 KGVSTRVYERA 136

## RESULT 12

US-09-834-366-17169  
; Sequence 17169, Application US/09834366  
; GENERAL INFORMATION:  
; APPLICANT: Bejani, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.052.REG  
; CURRENT APPLICATION NUMBER: US/09/834,366  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/197,873  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17169  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 62  
; OTHER INFORMATION: Xaa = Asp,Glu  
; NAME/KEY: UNSURE  
; LOCATION: 82  
; OTHER INFORMATION: Xaa = Lys,Asn  
US-09-834-366-17169

Query Match 96.1%; Score 649; DB 22; Length 129;  
Best Local Similarity 98.4%; Pred. No. 1.7e-64;  
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
| | | | | | | | | |  
Db 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60  
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEVCVM 120  
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Db 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEVCVM 120  
QY 121 KGVSTRVY 129  
| | | | | | | | | |  
Db 121 KGVSTRVY 129

## RESULT 13

US-60-197-873-17169  
; Sequence 17169, Application US/60197873  
; GENERAL INFORMATION:  
; APPLICANT: Bejani, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.US1.PRO  
; CURRENT APPLICATION NUMBER: US/60/197,873  
; CURRENT FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17169  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:14:58 ; Search time 11.74 Seconds  
(without alignments)  
390.957 Million cell updates/sec

Title: US-09-905-235-1  
Perfect score: 675  
Sequence: 1 MCDFAFGTGWKLYSSENFDDY.....KLVVECMKGVSTRVYERA 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 160442 seqs, 34771459 residues

Total number of hits satisfying chosen parameters: 160442

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA\_New:\*

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2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pap:\*

3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pap:\*

4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pap:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	69.0	133	5	US-09-901-436-7
2	463	68.6	132	5	US-09-901-436-11
3	449	66.5	133	5	US-09-901-436-10
4	445	65.9	132	5	US-09-986-240-2
5	399	59.1	132	5	US-09-971-187-2
6	225	33.3	134	5	US-09-901-436-9
7	212	31.4	135	5	US-09-901-436-8
8	201.5	29.9	138	6	US-10-017-754-328
9	122	18.1	107	5	US-09-901-436-2
10	86	12.7	127	5	US-09-981-353-21
11	74.5	11.0	304	5	US-09-620-394B-4280
12	74.5	11.0	547	5	US-09-708-427-20771
13	74.5	11.0	559	5	US-09-708-427-20770
14	74.5	11.0	610	5	US-09-815-242-13176
15	74.5	11.0	662	5	US-09-708-427-21666
16	69.5	10.3	380	5	US-09-708-427-21665
17	69.5	10.3	446	5	US-09-708-427-21665
18	69.5	10.3	510	5	US-09-708-427-21664
19	69	10.2	380	5	US-09-708-427-35496
20	69	10.2	446	5	US-09-708-427-35495
21	69	10.2	510	5	US-09-979-776-2
22	69	10.2	511	5	US-09-708-427-35494
23	68	10.1	2470	7	US-60-337-358-579
24	67.5	10.0	240	5	US-09-815-242-13453
25	67.5	10.0	241	5	US-09-815-242-13609
26	67.5	10.0	361	5	US-09-708-427-58892

27	67.5	10.0	365	5	US-09-708-427-58891
28	67.5	10.0	367	5	US-09-708-427-58890
29	67.5	10.0	602	5	US-09-815-242-10802
30	67	9.9	237	7	US-60-318-677-20
31	67	9.9	339	5	US-09-708-427-15957
32	67	9.9	342	5	US-09-708-427-15956
33	67	9.9	399	5	US-09-708-427-15955
34	65.5	9.7	181	5	US-09-995-493-38
35	65.5	9.7	263	5	US-09-708-427-1236
36	65.5	9.7	306	5	US-09-708-427-1235
37	65.5	9.7	357	5	US-09-708-427-1234
38	65.5	9.7	591	5	US-09-815-242-10419
39	65.5	9.7	856	5	US-09-708-427-15247
40	65.5	9.7	888	5	US-09-708-427-15246
41	65.5	9.7	1021	5	US-09-708-427-15245
42	65	9.6	206	5	US-09-815-242-10335
43	65	9.6	454	5	US-09-708-427-18105
44	65	9.6	522	5	US-09-708-427-18104
45	65	9.6	539	5	US-09-708-427-18103

## ALIGNMENTS

RESULT 1  
US-09-901-436-7  
; Sequence 7, Application US/09901436  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
;     Gentz, Reiner  
;     Yu, Guo-Liang  
;     Rosen, Craig A  
; TITLE OF INVENTION: Cytostatin I  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
;     ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
;     STREET: 9410 KEY WEST AVENUE  
;     CITY: ROCKVILLE  
;     STATE: MARYLAND  
;     COUNTRY: USA  
;     ZIP: 20850  
; COMPUTER READABLE FORM:  
;     MEDIUM TYPE: Floppy disk  
;     COMPUTER: IBM PC compatible  
;     OPERATING SYSTEM: PC-DOS/MS-DOS  
;     SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/901,436  
; APPLICATION NUMBER DATA:  
;     FILING DATE: 10-Jul-2001  
;     CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
;     APPLICATION NUMBER: 09/361,737  
;     FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
;     NAME: Wales, Michele M.  
;     REGISTRATION NUMBER: P-43,975  
;     REFERENCE/DOCKET NUMBER: PF175D2  
; TELECOMMUNICATION INFORMATION:  
;     TELEPHONE: 301-610-5772  
;     TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 7:  
;     SEQUENCE CHARACTERISTICS:  
;         LENGTH: 133 amino acids  
;         TYPE: amino acid  
;         STRANDEDNESS: single  
;         TOPOLOGY: linear  
;     MOLECULE TYPE: protein  
;     SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-901-436-7  
Query Match 69.0%; Score 466; DB 5; Length 133;  
Best Local Similarity 67.9%; Pred. No. 2.6e-38;

Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MDAFVGTWKLVSSENFDYMKYGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
 Db 1 MADAFVGTWKLVDKSNFDYMKSLGVGFATRKVASMTKPTTIIIEKNGDTITIKTQSTFKN 60  
 Qy 61 TEISFILGQEFDEVTAADRKKVSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLWVECV 120  
 Db 61 TEINFGIEFEDEVTAADRKKVSLVTLDDGKLIHVQKNGOETTLTRELVDGKLILTLTH 120  
 Qy 121 KGVSTRYER 131  
 Db 121 GSVSTRYER 131

RESULT 2

US-09-901-436-11

; Sequence 11, Application US/09901436

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; Gentz, Reiner

; Yu, Guo-Liang

; Rosen, Craig A

; TITLE OF INVENTION: Cytostatin I

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/901,436

; FILING DATE: 10-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/361,737

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: P-43,975

; REFERENCE/DOCKET NUMBER: PF175D2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-610-5772

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 132 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-901-436-11

Query Match 68.6%; Score 463; DB 5; Length 132;

Best Local Similarity 67.2%; Pred. No. 5e-38;

Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MDAFVGTWKLVSSENFDYMKYGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
 Db 1 MSNFGTWKLVSSENFDYMKALGVGATRKGLMARTVLIISKGDIIIRIESTFKN 60

Qy 61 TEISFILGQEFDEVTAADRKKVSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLWVECV 120  
 Db 61 TEISFKLGQEFEEETADNRKTSIVTLQSGSLNQVQRWDGKETTIIKKRLVNGKVAECKM 120

Qy 121 KGVSTRYER 131  
 Db 121 KGVCTRTRYER 131

RESULT 3

US-09-901-436-10

; Sequence 10, Application US/09901436

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; Gentz, Reiner

; Yu, Guo-Liang

; Rosen, Craig A

; TITLE OF INVENTION: Cytostatin I

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/901,436

; FILING DATE: 10-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/361,737

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: P-43,975

; REFERENCE/DOCKET NUMBER: PF175D2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-610-5772

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 133 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-901-436-10

Query Match 66.5%; Score 449; DB 5; Length 133;

Best Local Similarity 64.9%; Pred. No. 1.2e-36;

Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MDAFVGTWKLVSSENFDYMKYGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60  
 Db 1 MVDAFGLTWKLVDKSNFDYMKSLGVGFATRKQVASMTKPTTIIIEKNGDILTKTHSTFKN 60

Qy 61 TEISFILGQEFDEVTAADRKKVSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLWVECV 120  
 Db 61 TEISFKLGVEFEDEVTAADRKKVSIIVTLDDGKLIHVQKWDGQETTLVRELIDGKLILTLTH 120

Qy 121 KGVSTRYER 131  
 Db 121 GTAVCTRTRYER 131

RESULT 4

US-09-986-240-2

; Sequence 2, Application US/09986240

```

: GENERAL INFORMATION:
: APPLICANT: Weigelt, Johan
: APPLICANT: Weigelt, Mats
: TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
: TITLE OF INVENTION: METHOD
: FILE REFERENCE: 13425-047001
: CURRENT APPLICATION NUMBER: US/09/986,240
: CURRENT FILING DATE: 2001-10-19
: PRIOR APPLICATION NUMBER: 60/243,626
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: SE 0003811-7
: PRIOR FILING DATE: 2000-10-20
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 132
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-986-240-2

```

[illegible]

```

RESULT      5
US-09-971-187-2
; Sequence 2, Application US/09971187
; GENERAL INFORMATION:
; APPLICANT: Jian Ni et al.
; TITLE OF INVENTION: Cytostatin II
; FILE REFERENCE: PF221D1
; CURRENT APPLICATION NUMBER: US/09/971,187
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/043,646
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/US95/12540
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: human
US-09-971-187-2

```

[illegible]

Db 121 GDVAVRHYEKA 132

RESULT 6  
US-09-901-436-9  
; Sequence 9, Application US/09901436  
; GENERAL INFORMATION:  
; APPLICANT: NI. Jian

TITLE OF INVENTION: Cyclostatin I  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 STREET: 9410 KEY WEST AVENUE  
 CITY: ROCKVILLE  
 STATE: MARYLAND  
 COUNTRY: USA  
 ZIP: 20850

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.30
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/09/901.436
8  FILING DATE: 10-Jul-2001
9  CLASSIFICATION: <Unknown>

```

```

/ TELEFAX: 301-309-8439
/
/ INFORMATION FOR SEQ ID NO: 9:
/
/   SEQUENCE CHARACTERISTICS:
/     LENGTH: 134 amino acids
/     TYPE: amino acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/
/   MOLECULE TYPE: protein
/
/   SEQUENCE DESCRIPTION: SEQ ID NO: 9:
/ US-09-901-436-9

```

Query Match	33.3%;	Score 225;	DB 5;	Length 134;
Best Local Similarity	38.6%;	Pred. No. 6.3e-15;		
Matches	49;	Conservative 27;	Mismatches 49;	Indels 2;
Gaps	1;			
QY	7	GTWKLYSSENFDDYMKVEVGFATRKVAGNAKNMIISVANGDVTIISSETFKNTETISFI	66	
Db	7	GTWEMSENENFEGYMKALDIDFATPKIAVRLTQTKVIDQGDNFKTKTSTFRNYDVDT	66	
QY	67	LGQEFDEVT--ADDRVKVSTITLDGGVLHVHQWGDGKSTTKRKRREDDKLWVECVMGKVT	124	
Db	67	VGVFEFDYTKSLDNRHVKALVTWEGDVLVCVQGEKENRGWKQWIEGDKLYLELTCGDQV	126	
QY	125	STRVYER	131	
Db	127	CROVEFKK	133	

RESULT 7  
US-09-901-436-8  
; Sequence 8, Application US/09901436  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian

Genzt, Reiner  
Yu, Guo-Liang  
Rosen, Craig A  
TITLE OF INVENTION: Cytostatin I  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/901,436  
FILING DATE: 10-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/361,737  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wales, Michele M.  
REGISTRATION NUMBER: P-43,975  
REFERENCE/DOCKET NUMBER: PF175D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5772  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 31.4%; Score 212; DB 5; Length 135;  
Best Local Similarity 35.7%; Pred. No. 1.2e-13;  
Matches 46; Conservative 34; Mismatches 47; Indels 2; Gaps 1;  
QY 5 FVGTWKLVSSENFDDYMKVGVGFATRK--VAGMAKNMIIISVNGDVITIKSESTFKNTEIS 64  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 5 FTGYKMLVNEFPEYLALDYNVALRKIANLLKPKDEIVQGDHMIIRTLSTFRNYMD 64  
QY 65 FILQGEFDE--VTADRRKVKSTITLDGVLVHVQKWDGKSTTKRKREDDKLVVECVNKG 122  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 65 FQVGKEFEEDLTGIDRRKCMKTVTSWDGDKLQCVQKGEGRGWTQWIEGDELHLEMRVEG 124  
QY 123 VTSTRVYER 131  
Db 125 VVCKQVFKK 133

RESULT 8  
US-10-017-754-328  
; Sequence 328, Application US/10017754  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Carter, Darrick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.

APPLICANT: McNabb, Andria  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.478C18  
CURRENT APPLICATION NUMBER: US/10/017,754  
CURRENT FILING DATE: 2001-10-29  
NUMBER OF SEQ ID NOS: 2004  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 328  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-017-754-328

Query Match 29.9%; Score 201.5; DB 6; Length 138;  
Best Local Similarity 32.4%; Pred. No. 1.3e-12;  
Matches 47; Conservative 23; Mismatches 46; Indels 29; Gaps 3;  
QY 5 FVGTWKLVSSENFDDYMKVGVGFATRK--VAGMAKNMIIISVNGDVITIKSESTFKNTE 62  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 4 FSGNWKIIRSENFEELKVLGVNVMRLKRIAAASKPAVEIKQEGDTFYIKTSTTVTFTE 63  
QY 63 ISFILQGEFDEVTADRRKVKSTITLDGVLVHVQKWDG-----KSTTIK 106  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 64 INFKVGEEPEEQTVGGRPKSLV-----KWSEKNKMWCEQKLLKGEGPKTSWTR 112  
QY 107 RKREDDKLVVECVNKGVTSTRVYER 131  
Db 113 ELTNDGELILMTADDVYCTRVYVR 137

RESULT 9  
US-09-901-436-2  
; Sequence 2, Application US/09901436  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; Yu, Guo-Liang  
; Rosen, Craig A  
TITLE OF INVENTION: Cytostatin I  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/901,436  
FILING DATE: 10-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/361,737  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Wales, Michele M.  
REGISTRATION NUMBER: P-43,975  
REFERENCE/DOCKET NUMBER: PF175D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5772  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

```

;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-901-436-2

```

	Query Match	18.18;	Score 122;	DB 5;	Length 107;
	Best Local Similarity	33.8%;	Pred. No. 4.7e-05;		
	Matches 23;	Conservative 20;	Mismatches 25;	Indels 0;	Gaps 0;
QY	7 GTWKLVSSENDDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVITIKESTFKNTEISFI	66			
	: : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :				
Dd	7 GYRFVSGKNMEDYLQALNI SLAVRKIALLLKPKEIEHQGNHMTVRTLSFTFNVTLQFD	66			
	: : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :				
QY	67 LGQEFDEV 74				
	: : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :				
Dd	67 VGVOKGEV 74				
	: : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :				

```

RESULT 10
US-09-981-353-21
; Sequence 21, Application US/09981353
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1282225CD1
US-09-981-353-21

```

```

Query Match      12.7% ; Score 86 ; DB 5 ; Length 127 ;
Best Local Similarity 26.0% ; Pred. No. 0.18 ;
Matches 26 ; Conservative 17 ; Mismatches 29 ; Indels 28 ; Gaps 3 ;

QY      4  AFVGTFKVLVSSNFDDYMKYGVGFATRKVAGMAKPNMIIISVNGDV----- 49
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2  SFSGYQLQSOENFEAFKAIGL-----PEELIQCKDKIKGVSEIVQNGKHKF 49
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      50  ITIKSESTFKNTEISFILQGFEDFVTDADDRKVKSTITLDG 89
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      50  FITIGS--KVIQNEFTVGECELETMTGKGVTVVQLEG 87
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 11
US-09-620-394B-4280
; Sequence 4280, Application US/09620394B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1067P
; CURRENT APPLICATION NUMBER: US/09/620,394B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9131
; SEQ ID NO 4280
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..304
; OTHER INFORMATION: xaa is any amino acid

```

```

; NAME/KEY: misc_feature
; LOCATION: 1..304
; OTHER INFORMATION: Ceres Seq. ID 1388881
US-09-620-394B-4280

```

Query Match	11.0%	Score	74.5	DB	5	Length	304
Best Local Similarity	25.0%	Pred. No.	7.3				
Matches	36	Conservative	19	Mismatches	54	Indels	35
Gaps							
QY	3	DAFVGTKWKLVSSENFDDYM	-KEVCGVG	FATPKVAGMAKPMIISV	GVNDVI	IKS-----	54
		:    :    :    :    :	:	:	:	:	
Db	152	EAFSGCTTIVSCKVATDHMG	QSGRGYGV	FQDTDKSAK	-NAIEKINGKLVNDKQI	FGVGF	210
		:    :    :    :    :	:	:	:	:	
QY	55	-----ESTFKNTEISFLTG	GEFFEDV	ATDRKVKSTITL	DGGV--LVHVQKWDGKS	-----	102
		:    :    :    :    :	:	:	:	:	
Db	211	RKEERESAADKMKPTNYV	VKNLSEAT	TDD-ELKTTFGQYGSIS	SAVVVRMDGDKGR	CR	269
		:    :    :    :    :	:	:	:	:	
QY	103	-----TTIKRKREDDK	113				
		:    :    :    :    :	:	:	:	:	
Db	270	VNFENPEDAARAVEALNG	KKFFD	DK			

```

RESULT 12
US-09-708-427-20771
; Sequence 20771, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20771
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..547
; OTHER INFORMATION: xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..547
; OTHER INFORMATION: Ceres Seq. ID 1838598
US-09-708-427-20771

```

[illegible]

RESULT 13  
US-09-708-427-20770  
; Sequence 20770, Application US/09708427  
; GENERAL INFORMATION:  
; APPLICANT: N. ALEXANDROV et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED  
; TITLE OF INVENTION: THERREY





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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 09:13:58 ; Search time 14.4 Seconds  
(without alignments)  
698.267 Million cell updates/sec

Title: US-09-905-235-1  
Perfect score: 675  
Sequence: 1 MCDFAVGTWKLVSSENFDDY.....KLVVECVMGVSTRVYERA 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 68.\*

- 1: pir1.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	132	1 FZHU1	fatty acid-binding
2	623	92.3	132	2 B25952	myelin P2 protein
3	578	85.6	132	2 S57744	adipocyte-type fat
4	486	72.0	132	1 MPR82	myelin P2 protein
5	477	70.7	133	2 A27452	fatty acid-binding
6	466	69.0	133	2 PC4011	fatty acid-binding
7	463	68.6	132	1 MPH02	myelin P2 protein
8	450	66.7	132	2 JH0407	myelin P2 protein
9	449	66.5	133	1 FZHU1	fatty acid-binding
10	448	66.4	131	1 FZHU1	myelin P2 protein
11	446	66.1	133	2 A34676	fatty acid-binding
12	425	63.0	131	2 S06479	fatty acid-binding
13	392	58.1	132	2 A49184	fatty acid-binding
14	390	57.8	132	2 I52524	testis lipid bindi
15	385	57.0	132	2 I56510	fatty acid-binding
16	381	56.4	132	2 I58161	lipid-binding prot
17	381	56.4	132	2 I48923	fatty acid-binding
18	378	56.0	132	2 S20297	fatty acid-binding
19	366	54.2	135	2 I56326	fatty acid-binding
20	362	53.6	135	2 A47497	lipid-binding prot
21	361	53.5	135	2 JC2201	fatty acid-binding
22	307.5	45.6	135	2 T15205	hypothetical prote
23	300.5	44.5	136	2 T15207	hypothetical prote
24	256.5	38.0	137	2 T25123	hypothetical prote
25	242.5	35.9	133	2 A48578	fatty acid-binding
26	231.5	34.3	134	2 S29600	fatty acid-binding
27	229.5	34.0	133	2 A39818	14K fatty acid-bin
28	227	33.6	133	2 A44870	fatty acid-binding
29	227	33.6	134	2 S34717	retinol-binding pr

30	225	33.3	134	2 A29065	retinol-binding pr
31	223	33.0	134	2 S45378	cellular retinol b
32	223	33.0	134	2 S43470	fatty-acid-binding
33	222	32.9	137	1 FZHU1	retinoic acid-bind
34	220	32.6	137	1 RJBOA	retinoic acid-bind
35	220	32.6	137	2 A35825	retinoic acid-bind
36	218	32.3	135	1 RJRTO	retinol-binding pr
37	212	31.4	135	1 RJHU0	retinol-binding pr
38	212	31.4	135	2 S16355	retinol-binding pr
39	206	30.5	134	2 S69360	retinol-binding pr
40	203.5	30.1	138	2 A42495	retinoic acid-bind
41	201.5	29.9	138	1 RJHU2	retinoic acid-bind
42	197.5	29.3	138	2 I51265	retinoic acid-bind
43	196	29.0	139	2 I53298	xCRABP - African c
44	191	28.3	95	2 A61629	cellular retinoic
45	190	28.1	132	1 FZHU1	retinoic acid-bind
					fatty acid-binding

ALIGNMENTS

RESULT 1  
FZHU1  
fatty acid-binding protein, adipocyte - human  
N:Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein  
C:Species: Homo sapiens (man)  
C:Date: 20-Dec-1989 #sequence\_revision 03-May-1996 #text\_change 22-Jun-1999  
C:Accession: A33363  
R:Baxa, C.A.; Sha, R.S.; Buel, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Bou  
Biochemistry 28, 8683-8690, 1989  
A:Title: Human adipocyte lipid-binding protein: purification of the protein and cloni  
A:Reference number: A33363; MUID:90105397  
A:Accession: A33363  
A:Molecule type: mRNA  
A:Residues: 1-132 <BAX>  
A:Cross-references: GB:J02874; NID:gl78346; PIDN:AAA51689.1; PID:gl78347  
A:Experimental source: subcutaneous fat  
C:Genetics:  
A:Gene: GDB:FABP4  
A:Cross-references: GDB:128030  
A:Map position: lp33-lp32  
C:Superfamily: myelin P2 protein  
C:Keywords: blocked amino end; lipid binding; phosphoprotein  
F:2/Modified site: blocked amino end (Cys) (in mature form) (probably acetylated) #st  
F:20/Binding site: phosphate (Tyr) (covalent) #status predicted  
F:127,129/Binding site: fatty acid (Arg, Tyr) #status predicted

Query Match	100.0%	Score	675	DB	1	Length	132
Best Local Similarity	100.0%	Pred. No.	1.6e-54				
Matches	132	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	MCDFAVGTWKLVSSENFDDYMKVEGVGFATPKVAGMAKPNMIISVNGDVTIKSESTFKN	60				
DB	1	MCDFAVGTWKLVSSENFDDYMKVEGVGFATPKVAGMAKPNMIISVNGDVTIKSESTFKN	60				
QY	61	TEISFILGQEFDEVTADRRKVKSTITLDGGVLHVQKWDGKSTIKRKREDKLVCEVM	120				
DB	61	TEISFILGQEFDEVTADRRKVKSTITLDGGVLHVQKWDGKSTIKRKREDKLVCEVM	120				
QY	121	KGVTSTRVYERA	132				
DB	121	KGVTSTRVYERA	132				

RESULT 2  
B25952  
myelin P2 protein homolog - mouse  
N:Alternate names: adipocyte lipid-binding protein; adipocyte P2 protein  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 31-Dec-2000  
C:Accession: B25952; PC1249; A24884; A05089; A30810; I49440; I49467  
R:Phillips, M.; Djan, P.; Green, H.

J. Biol. Chem. 261, 10821-10827, 1986  
A:Title: The nucleotide sequence of three genes participating in the adipose differentiation  
A:Reference number: A92553; MUID:86278164  
A:Accession: B25952  
A:Molecule type: DNA  
A:Residues: 1-132 <PHI>  
A:Cross-references: GB:M13385; NID:g198718; PIDN:AAA39417.1; PID:g387401  
A:Note: the authors translated the codon GTG for residue 111 as Gly  
R:Bansal, M.P.; Medina, D.  
Biochem. Biophys. Res. Commun. 191, 61-69, 1993  
A:Title: Expression of fatty acid-binding proteins in the developing mouse mammary gland  
A:Reference number: PC1248; MUID:93191717  
A:Accession: PC1249  
A:Molecule type: protein  
A:Residues: 25-35; 37-51; 59-88 <BAN>  
A:Experimental source: mammary gland  
R:Hunt, C.R.; Ro, J.H.S.; Dobson, D.E.; Min, H.Y.; Spiegelman, B.M.  
Proc. Natl. Acad. Sci. U.S.A. 83, 3786-3790, 1986  
A:Title: Adipocyte P2 gene: Developmental expression and homology of 5'-flanking sequence  
A:Reference number: A24884; MUID:86233319  
A:Accession: A24884  
A:Molecule type: DNA  
A:Residues: 1-39, 'T', '41-110, 'G', 112-132 <HUN>  
A:Cross-references: GB:M13264; NID:g200183; PIDN:AAA39870.1; PID:g387504  
A:Note: the authors translated the codon ACC for residue 40 as Ser  
R:Bernlohr, D.A.; Angus, C.W.; Lane, M.D.; Bolanowski, M.A.; Kelly Jr., T.J.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5468-5472, 1984  
A:Title: Expression of specific mRNAs during adipose differentiation: identification of  
A:Reference number: A05089; MUID:84298159  
A:Accession: A05089  
A:Molecule type: mRNA  
A:Residues: 1-110, 'G', 112-132 <BER>  
A:Cross-references: GB:K02109; NID:g198716; PIDN:AAA39416.1; PID:g293695  
R:Matarse, V.; Bernlohr, D.A.  
J. Biol. Chem. 263, 14544-14551, 1988  
A:Title: Purification of murine adipocyte lipid-binding protein. Characterization as a  
A:Reference number: A30810; MUID:89008309  
A:Accession: A30810  
A:Molecule type: protein  
A:Residues: 2-110, 'G', 112-132 <MAT>  
R:Cook, K.S.; Hunt, C.R.; Spiegelman, B.M.  
J. Cell Biol. 100, 514-520, 1985  
A:Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcriptional  
A:Reference number: I49440; MUID:85105214  
A:Accession: I49440  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 11-110, 'G', 112-132 <RES>  
A:Cross-references: GB:M28726; NID:g191492; PIDN:AAA37112.1; PID:g191493  
R:Cook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.; Lan  
Proc. Natl. Acad. Sci. U.S.A. 85, 2949-2953, 1988  
A:Title: Expression of the differentiation-induced gene for fatty acid-binding protein  
A:Reference number: I49467; MUID:88203618  
A:Accession: I49467  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-11 <RES>  
A:Cross-references: GB:M20497; NID:g191743; PIDN:AAA37188.1; PID:g191744  
A:Experimental source: 3T3-L1 cells  
C:Genetics:  
A:Introns: 25/1; 82/3; 116/3  
C:Superfamily: myelin P2 protein  
C:Keywords: lipid binding; phosphoprotein

Query Match 92.3%; Score 623; DB 2; Length 132;  
Best Local Similarity 91.7%; Pred. No. 8.6e-50;  
Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVTIKSESTFKN 60  
Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVTIKSESTFKN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKRRKDDKLWVECV 120  
Db 61 TEISFLGLGVFEDEITADDRKVKSIITLDGALVQVQKWDGKSTTIKRRKDDKLWVECV 120  
Qy 121 KGVTSRTRYERA 132  
Db 121 KGVTSRTRYERA 132  
RESULT 3  
S57744  
adipocyte-type fatty acid binding protein - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 13-Aug-1999  
C:Accession: S57744  
R:Specht, B.; Bartetzko, N.; Kuhl, H.; Franke, R.; Boerchers, T.; Spener, F.  
submitted to the EMBL Data Library, June 1995  
A:Description: Mammary derived growth inhibitor - not a distinct protein but a mix of  
A:Reference number: S57744  
A:Accession: S57744  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <SPE>  
A:Cross-references: EMBL:X89244; NID:g895753; PIDN:CAA61532.1; PID:g895754  
C:Superfamily: myelin P2 protein

Query Match 85.6%; Score 578; DB 2; Length 132;  
Best Local Similarity 84.1%; Pred. No. 1.1e-45;  
Matches 111; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVTIKSESTFKN 60  
Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVTIKSESTFKN 60  
Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKRRKDDKLWVECV 120  
Db 61 TEISFLGLGVFEDEITADDRKVKSIITLDGALVQVQKWDGKSTTIKRRKDDKLWVECV 120  
Qy 121 KGVTSRTRYERA 132  
Db 121 NGVTATRYERA 132  
RESULT 4  
MPRB2  
myelin P2 protein - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Jun-1980 #sequence\_revision 10-May-1996 #text\_change 22-Jun-1999  
C:Accession: A28081; A92266; A92372; A03145  
R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.  
J. Biol. Chem. 263, 8332-8337, 1988  
A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.  
A:Reference number: A28081; MUID:88228063  
A:Accession: A28081  
A:Molecule type: mRNA  
A:Residues: 1-132 <NAR>  
A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658  
A:Note: translation of initiator Met is not shown  
R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.  
J. Biol. Chem. 255, 1058-1063, 1980  
A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.  
A:Reference number: A92266; MUID:80094496  
A:Accession: A92266  
A:Molecule type: protein  
A:Residues: 2-56 <ISI>  
R:Ishaque, A.; Hofmann, T.; Eylar, E.H.  
J. Biol. Chem. 257, 592-595, 1982  
A:Title: The complete amino acid sequence of the rabbit P2 protein.  
A:Reference number: A92372; MUID:82098098  
A:Accession: A92372  
A:Molecule type: protein  
A:Residues: 56-72, 'Q', '74-83, 'T', '85-98, 'N', 100-132 <IS2>

A;Residues: 2-10;46-53 <GIB>

**A/Title:** Expression of fatty acid-binding proteins in the developing mouse mammary gland





Qy 121 KGVSTRVYER 131  
 Db 121 GTAVCTRYEK 131

RESULT 12  
 S06479  
 fatty acid-binding protein, brain - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 24-Nov-1999  
 C:Accession: S06479; JH0198  
 R:Schoentgen, F.; Pignede, G.; Bonanno, L.M.; Jolles, P.  
 Eur. J. Biochem. 185, 35-40, 1989  
 A:Title: Fatty acid-binding protein from bovine brain. Amino acid sequence and some prop  
 A:Reference number: S06479; MUID:90032683  
 A:Accession: S06479  
 A:Molecule type: protein  
 A:Residues: 1-131 <SCH>  
 A:Experimental source: brain  
 A:Note: 11-Val, 12-Asp, 14-Lys, 18-Asp, 33-Ala, 34-Ser, 40-Thr, 43-Glu, 44-Lys, 49-Val,  
 R:Schoentgen, F.; Bonanno, L.M.; Pignede, G.; Jolles, P.  
 Mol. Cell. Biochem. 98, 35-39, 1990  
 A:Title: Amino acid sequence and some ligand binding properties of fatty acid-binding pr  
 A:Reference number: JH0198; MUID:91094811  
 A:Contents: annotation  
 C:Comment: Synaptosomal Na<sup>+</sup>-dependent amino acid transport is stimulated by the fatty ac  
 C:Superfamily: myelin P2 protein  
 C:Keywords: blocked amino end  
 F:1/Modified site: blocked amino end (Val) (probably acetylated) #status experimental

Query Match 63.0%; Score 425; DB 2; Length 131;  
 Best Local Similarity 62.0%; Pred. No. 8.8e-32;  
 Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIITIKSEPFKTE 62  
 Db 2 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIITIKSEPFKTE 61

Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 122  
 Db 62 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 121

Qy 123 VTSTRVYER 131  
 Db 122 VVAVRHYEK 130

RESULT 13  
 A49184  
 fatty acid-binding protein - chicken  
 N:Alternate names: lipid-binding protein  
 C:Species: Gallus gallus (chicken)  
 C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 13-Aug-1999  
 C:Accession: A49184; S26599  
 R:Godbout, R.  
 Exp. Eye Res. 56, 95-106, 1993  
 A:Title: Identification and characterization of transcripts present at elevated levels i  
 A:Reference number: A49184; MUID:93162137  
 A:Accession: A49184  
 A:Molecule type: mRNA  
 A:Status: preliminary  
 A:Residues: 1-132 <GOD>  
 A:Cross-references: EMBL:X65459; NID:963230; PIDN:CAA46451.1; PID:g63231  
 A:Experimental source: retina  
 A:Note: sequence extracted from NCBI backbone (NCBIP:124757)  
 C:Superfamily: myelin P2 protein

Query Match 58.1%; Score 392; DB 2; Length 132;  
 Best Local Similarity 56.1%; Pred. No. 8.9e-29;  
 Matches 74; Conservative 19; Mismatches 39; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKN 60  
 Db 1 MVEAFCAWKALADSHNDFDEYMKALGVGFAMRQVGNVTKPTVLIISSEGDKVIRIQSTFKN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120  
 Db 61 TEISFKLGEFEETTPDDRCKSVVTLDDGKLHVQKWDGKSTTIKKRREDDKLVEECVM 120

Qy 121 KGVSTRVYER 132  
 Db 121 GDVVAVRHYEK 132

RESULT 14  
 I52524  
 testis lipid binding protein - rat  
 N:Alternate names: 15 kDa perforatorial protein PERF 15  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 13-Aug-1999  
 C:Accession: I52524; I53089  
 R:Schmitt, M.C.; Jamison, R.S.; Orgebin-Crist, M.C.; Ong, D.E.  
 Biol. Reprod. 51, 239-245, 1994  
 A:Title: A novel, testis-specific member of the cellular lipophilic transport protein  
 A:Reference number: I52524; MUID:95035569  
 A:Accession: I52524  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-132 <RES>  
 A:Cross-references: EMBL:U07870; NID:g469051; PIDN:AAA68627.1; PID:g469052  
 R:Oko, R.J.; Morales, C.C.; Oki, R.; Morales, C.R.  
 Dev. Biol. 166, 235-245, 1994  
 A:Title: A novel testicular protein, with sequence similarities to a family of lipid  
 A:Reference number: I53089; MUID:95046905  
 A:Accession: I53089  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-132 <RES>  
 A:Cross-references: EMBL:U09022; NID:g538268; PIDN:AAA67873.1; PID:g538269  
 C:Superfamily: myelin P2 protein

Query Match 57.8%; Score 390; DB 2; Length 132;  
 Best Local Similarity 56.5%; Pred. No. 1.4e-28;  
 Matches 74; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKN 60  
 Db 1 MIEPFLGTWKLVSSENFENYRELVECEPRKVAELIKPSVISFNGERMIDQAGSACRN 60

Qy 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120  
 Db 61 TEISFKLGEFEETTPDDRCKSVVTLDDGKLHVQKWDGKSTTIKKRREDDKLVEECVM 120

Qy 121 KGVSTRVYER 131  
 Db 121 NNVTSTRTYER 131

RESULT 15  
 I56510  
 fatty acid binding protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 13-Aug-1999  
 C:Accession: I56510  
 R:Bennett, E.; Stenvers, K.L.; Lund, P.K.; Popko, B.  
 J. Neurochem. 63, 1616-1624, 1994  
 A:Title: Cloning and characterization of a cDNA encoding a novel fatty acid binding p  
 A:Reference number: I56510; MUID:95016702  
 A:Accession: I56510  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-132 <RES>

A:Cross-references: EMBL:U02096; NID:g476081; PIDN:AAA60455.1; PID:g476082  
C:Superfamily: myelin P2 protein

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Query Match      57.0%; Score 385; DB 2; Length 132;
Best Local Similarity 55.3%; Pred. No. 3.9e-28;
Matches 73; Conservative 19; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYKKEVGVGFPATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
Db 1 MVDAFCATWKLTDSONFDEYKALGVGFATRGVGNVTKPTVIISQEGGKWIQTCTFKN 60

Qy 61 TEISFILGGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKREDDKLVECVN 120
Db 61 TEISFQLGEEFEETSIDDRNCKSVIRLDGDKLIHVQKWDGKRETCVREIKDGKVVVTLTF 120

Qy 121 KGVTSRVYERA 132
Db 121 GDVVAVRCYKA 132
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Search completed: January 24, 2002, 09:16:01  
Job time: 123 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:15:23 ; Search time 11.7 Seconds  
(without alignments)  
413.654 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MCDFAVGTVKLVSSSENFDDY.....KLVVECVKGVTVSTRYERA 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	670	99.3	131	1 FABA_HUMAN	P15090 homo sapien
2	620	91.9	131	1 FABA_MOUSE	P04117 mus musculus
3	608	90.1	131	1 FABA_PIG	P07788 sus scrofa
4	607	89.9	131	1 FABA_RAT	P70623 rattus norv
5	573	84.9	131	1 FABA_BOVIN	P48035 bos taurus
6	482	71.4	131	1 MYP2_RABIT	P02691 oryctolagus
7	472	69.9	132	1 FABH_RAT	P07483 rattus norv
8	466	69.0	132	1 FABH_MOUSE	P11404 mus musculus
9	459	68.0	131	1 MYP2_HUMAN	P02689 homo sapien
10	448	66.4	131	1 MYP2_BOVIN	P02690 bos taurus
11	446	66.1	131	1 MYP2_MOUSE	P24526 mus musculus
12	445	65.9	132	1 FABH_HUMAN	P05413 homo sapien
13	442	65.5	132	1 FABH_BOVIN	P10790 bos taurus
14	442	65.5	132	1 FABH_PIG	P02772 sus scrofa
15	425	63.0	131	1 FABB_BOVIN	P09139 bos taurus
16	424	62.8	132	1 FABB_MOUSE	P01308 oncorhynch
17	395	58.5	131	1 FABB_HUMAN	O15540 homo sapien
18	390	57.8	132	1 TLBP_RAT	P55054 rattus norv
19	388	57.5	131	1 FABB_CHICK	P05423 gallus gall
20	386	57.2	132	1 TLBP_MOUSE	P08716 mus musculus
21	381	56.4	131	1 FABB_RAT	P55051 rattus norv
22	378	56.0	132	1 FABL_GINGI	P80049 ginglymosto
23	377	55.9	131	1 FABB_MOUSE	P51880 mus musculus
24	367	54.4	135	1 FABB_BOVIN	P55052 bos taurus
25	366	54.2	135	1 FABB_HUMAN	Q01469 homo sapien
26	362	53.6	135	1 FABB_MOUSE	Q05816 mus musculus
27	361	53.5	135	1 FABB_RAT	P55053 rattus norv
28	326	48.3	114	1 FABL_LAMJA	P82188 lampetra ja
29	270.5	40.1	133	1 FABB_ECHGR	Q02970 echinococcu
30	250	37.0	131	1 FABB_LEPDS	Q9u5p1 lepidoglyph
31	238	35.3	130	1 FABB_BLOTA	Q17284 blomia trop
32	229.5	34.0	133	1 FABB_SCHMA	P29498 schistosoma
33	227	33.6	133	1 FABB_SCHGR	P41496 schistocerc

34	227	33.6	133	1 RET2_MOUSE	Q08652 mus musculus
35	225	33.3	133	1 RET2_HUMAN	P50120 homo sapien
36	225	33.3	133	1 RET2_RAT	P06768 rattus norv
37	223	33.0	133	1 RET2_PIG	P50121 sus scrofa
38	222	32.9	136	1 RET3_HUMAN	P29762 homo sapien
39	221	32.7	133	1 FABM_LOEMI	P41509 locusta mig
40	220	32.6	136	1 RET3_BOVIN	P02695 bos taurus
41	218	32.3	134	1 RET1_RAT	P02696 rattus norv
42	215	31.9	136	1 RET3_FUGRU	O42386 fugu rubrip
43	212	31.4	134	1 RET1_HUMAN	P09455 homo sapien
44	212	31.4	134	1 RET1_MOUSE	Q00915 mus musculus
45	206.5	30.6	137	1 RET4_MOUSE	P22935 mus musculus

ALIGNMENTS

RESULT 1					
FABA_HUMAN					
ID	FABA_HUMAN	STANDARD;	PRT;	131 AA.	
AC	P15090;				
DT	01-APR-1990 (Rel. 14, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING PROTEIN) (ALBP) (A-FABP).				
GN	FABP4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90105397; PubMed=2481498;				
RA	Baxa C.A., Sha R.S.; Buel M.K., Smith A.J., Matarese V.,				
RA	Chinander L.L., Boundy K.L., Bernlohr D.A.;				
RT	"Human adipocyte lipid-binding protein: purification of the protein and cloning of its complementary DNA.";				
RL	Biochemistry 28:8683-8690(1989).				
CC	-1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG CHAIN FATTY ACID AND RETINOIC ACID.				
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).				
CC	-1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; J02874; AAA51689.1; --				
DR	PIR; A33363; A33363.				
DR	HSSP; P04117; IALB.				
DR	MIM; 600434; --				
DR	InterPro; IPR000463; Fatty_acid_BP.				
DR	InterPro; IPR000566; Lipoclin_cycFABP.				
DR	Protein; P00061; Lipocalin; 1.				
DR	PRINTS; PR00178; FATTYACIDBP.				
DR	PROSITE; PS00214; FABP; 1.				
KW	Transport; Lipid-binding; Phosphorylation.				
FT	INIT MET 0 19				
FT	MOD_RES 19 19				
FT	BY SIMILARITY.				
FT	PHOSPHORYLATION (BY TYR-KINASES) (BY SIMILARITY).				
SQ	SEQUENCE 131 AA; 14588 MW; 81C241B63DD98235 CRC64;				

Query Match 99.3%; Score 670; DB 1; Length 131;  
Best Local Similarity 100.0%; Pred. No. 2.5e-53;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	CDAPVGTWKLVSSENFDDTHKVEGVGFATRKVAGMAKPNMIISVNGDVITTKSSTFKNT	61
Db	1	CDAPVGTWKLVSSENFDDTHKVEGVGFATRKVAGMAKPNMIISVNGDVITTKSSTFKNT	60
Qy	62	EISFILGOEFDVTDADRKVKSTITLDGGVLVHVQKDGKSTTIKKRDKLVVEVCVMK	121
Db	61	EISFILGOEFDVTDADRKVKSTITLDGGVLVHVQKDGKSTTIKKRDKLVVEVCVMK	120
Qy	122	GVTSTRVYERA 132	
Db	121	GVTSTRVYERA 131	
RESULT 2			
FABA_MOUSE STANDARD; PRT; 131 AA.			
ID	AC	P04117;	
DT	01-NOV-1986	(Rel. 03, Created)	
DT	01-NOV-1990	(Rel. 16, Last sequence update)	
DT	20-AUG-2001	(Rel. 40, Last annotation update)	
DE	FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFAPB) (ADIPOCYTE LIPID-BINDING		
DE	PROTEIN) (ALBP) (P2 ADIPOCYTE PROTEIN) (MYELIN P2 PROTEIN HOMOLOG)		
DE	(3T3-L1 LIPID BINDING PROTEIN) (422 PROTEIN) (P15).		
GN	FABPA OR AP2		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
LN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84298159; PubMed=6206497;		
RA	Bernlohr D.A., Angus C.W., Lane M.D., Bolanowski M.A., Kelly T.J. Jr.;		
RA	"Expression of specific mRNAs during adipose differentiation:		
RT	Identification of an mRNA encoding a homologue of myelin P2		
RT	protein.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).		
LN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=86278164; PubMed=3520554;		
RA	Hunt C.R., Ro J.H.-S., Dobson D.E., Min H.Y., Spiegelman B.M.;		
RA	"Adipocyte P2 gene: developmental expression and homology of		
RT	5'-flanking sequences among fat cell-specific genes.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 83:3786-3790(1986).		
LN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=86278164; PubMed=3015943;		
RA	Phillips M., Djian P., Green H.;		
RA	"The nucleotide sequence of three genes participating in the adipose		
RT	differentiation of 3T3 cells.";		
RL	J. Biol. Chem. 261:10821-10827(1986).		
LN	[4]		
RP	SEQUENCE OF 1-10 FROM N.A.		
RX	MEDLINE=88203618; PubMed=2452440;		
RA	Cook J.S., Lucas J.J., Sibley E., Bolanowski M.A., Christy R.J.,		
RA	Kelly T.J. Jr., Lane M.D.;		
RA	"Expression of the differentiation-induced gene for fatty acid-binding		
RT	protein is activated by glucocorticoid and CAMP.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 85:2949-2953(1988).		
LN	[5]		
RP	SEQUENCE		
RX	MEDLINE=89008309; PubMed=2844775;		
RA	Matarese V., Bernlohr D.A.;		
RA	"Purification of murine adipocyte lipid-binding protein.		
RT	Characterization as a fatty acid- and retinoic acid-binding		
RT	protein.";		
RL	J. Biol. Chem. 263:14544-14551(1988).		
LN	[6]		
RP	SEQUENCE OF 10-131 FROM N.A.		
RX	MEDLINE=85105214; PubMed=3968175;		
RA	Cook K.S., Hunt C.R., Spiegelman B.M.;		
RA	"Developmentally regulated mRNAs in 3T3-adipocytes: analysis of		
RT	transcriptional control.";		
RL	J. Cell Biol. 100:514-520(1985).		

FT STRAND 59 64  
 FT TURN 66 67  
 FT STRAND 70 73  
 FT TURN 75 76  
 FT STRAND 79 87  
 FT TURN 88 89  
 FT STRAND 90 97  
 FT TURN 98 99  
 FT STRAND 100 109  
 FT TURN 110 111  
 FT STRAND 112 119  
 FT TURN 120 121  
 FT STRAND 122 130  
 SQ SEQUENCE 131 AA; ED57D4E2774B8E32 CRC64;

Query Match 91.9%; Score 620; DB 1; Length 131;  
 Best Local Similarity 91.6%; Pred. No. 7.2e-49;  
 Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 CDAFVGTVKLVSSNFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 61  
 DB 1 CDAFVGTVKLVSSNFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 60

QY 62 EISFILGOEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKRRDDKLVVECVMK 121  
 DB 61 EISFKLGVFEDEVTADDRKVKSTITLDGGALVQKWDGKSTTIKRRDGDGLVVECVMK 120

QY 122 GVTSTRYVERA 132  
 DB 121 GVTSTRYVERA 131

RESULT 3  
 FABA\_PIG ID FABA\_PIG STANDARD; PRT; 131 AA.  
 AC Q97788;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING  
 DE PROTEIN) (ALBP) (A-FABP) (AP2).  
 GN FAPB4.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=DUCOC; TISSUE=Liver;  
 RX MEDLINE=99099248; PubMed=9880671;  
 RA Gerbens F., Jansen A., van Erp A.J.M., Harders F., Meuwissen T.H.E.,  
 RA Rettenberger G.F.W., Veerkamp J.H., te Pas M.F.W.;  
 RT "The adipocyte fatty acid-binding protein locus: characterization and  
 RT association with intramuscular fat content in pigs.";  
 RL Mamm. Genome 9:1022-1026(1998).  
 RN [2]  
 RP SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.  
 RC TISSUE=Fat;  
 RX MEDLINE=90241143; PubMed=2334399;  
 RA Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;  
 RT "The purification and characterization of a fatty acid binding protein  
 RT specific to pig (Sus domesticus) adipose tissue.";  
 RL Biochem. J. 267:373-378(1990).  
 CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG  
 CC CHAIN FATTY ACID AND RETINOIC ACID.  
 CC -1- FUNCTION: INVOLVED IN THE REGULATION OF INTRAMUSCULAR FAT  
 CC ACCRETION.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: ADIPOSE TISSUE.  
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.  
 CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF  
 CC TRANSPORTER.

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 CC -----  
 CC EMBL; Y16039; CAA75995.1; -;  
 CC HSP; P04117; ILID  
 CC InterPro; IPR000463; Fatty\_acid\_BP.  
 CC InterPro; IPR000566; Lipocalin\_cytrFABP.  
 CC Pfam; PF00061; lipocalin; 1.  
 CC PRINTS; PR00178; FATTYACIDBP.  
 CC PROSITE; PS00214; FABP; 1.  
 CC Transport; Lipid-binding; Phosphorylation;  
 CC INT\_MET 0  
 CC MOD\_RES 19 19  
 CC PHOSPHORYLATION (BY TYR-KINASES)  
 CC (BY SIMILARITY).  
 CC SEQUENCE 131 AA; 14545 MW; 656CB0CA08CD4AB2 CRC64;  
 CC -----  
 CC Query Match 90.1%; Score 608; DB 1; Length 131;  
 CC Best Local Similarity 88.5%; Pred. No. 8.4e-48;  
 CC Matches 116; Conservative 9; Mismatches 6; Indels 0; Gaps 0;  
 CC -----  
 CC QY 2 CDAFVGTVKLVSSNFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 61  
 CC DB 1 CDAFVGTVKLVSSNFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 60

QY 62 EISFILGOEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKRRDDKLVVECVMK 121  
 DB 61 EIAFKLGOEFDEVTADDRKVKSTITLDGGALVQKWDGKSTTIKRRIVDKLVVECVMK 120

QY 122 GVTSTRYVERA 132  
 DB 121 GVTATRIYERA 131

RESULT 4  
 FABA\_RAT ID FABA\_RAT STANDARD; PRT; 131 AA.  
 AC P70623;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING  
 DE PROTEIN) (ALBP).  
 GN FAPB4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Prinsen C., Veerkamp J.H.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG  
 CC CHAIN FATTY ACID AND RETINOIC ACID.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF  
 CC TRANSPORTERS.  
 CC -----  
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 CC -----  
 CC EMBL; U75581; AAB18344.1; -.

DR HSP: P04117; 1ALB.  
DR InterPro: IPR000463; Fatty acid BP.  
DR InterPro: IPR000566; Lipocalin; 1.  
DR Pfam: PF00061; lipocalin; 1.  
DR PRINTS; PR00178; FATTYACIDBP.  
DR PROSITE; PS00214; FAMP; 1.  
KW Transport; Lipid-binding; Phosphorylation.  
FT INIT\_MET 0 BY SIMILARITY.  
FT MOD\_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)  
FT SEQUENCE 131 AA; 14577 MW; 5228D0AC14FFD23B CRC64;  
FT MOD\_RES 19 19 BY SIMILARITY.  
FT INIT\_MET 0 BY SIMILARITY.  
FT MOD\_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)  
FT SEQUENCE 131 AA; 14577 MW; 5228D0AC14FFD23B CRC64;  
Query Match 89.98; Score 607; DB 1; Length 131;  
Best Local Similarity 88.58; Pred. No. 1e-47; 7; Indels 0; Gaps 0;  
Matches 116; Conservative 8; Mismatches 8; Indels 0; Gaps 0;  
QY 2 CDAFVGWTKLVSSSENFDDYMEKVGFGFATRKVAGMAKPNLIISVNGDVITIKSESTFKNT 61  
DB 1 CDAFVGWTKLVSSSENFDDYMEKVGFGFATRKVAGMAKPNLIISVNGDVITIKSESTFKNT 60  
QY 62 EISFILGQEFDEVTDARRKVKSTITLGGVLVHVQKWDGKSTTKRKREDDKLVVECYMK 121  
DB 61 EISFKLGVEFEITPDDRKVKSIITLGGVLVHVQKWDGKSTTKRKREDDKLVVECYMK 120  
QY 122 GVTSTRYVERA 132  
DB 121 GVTSTRYVERA 131  
RESULT 5  
FABA\_BOVIN  
ID FABA\_BOVIN STANDARD; PRT; 131 AA.  
AC P48035;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING PROTEIN) (ALBP).  
GN FABP4.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=96355299; PubMed=8702709;  
RA Specht B., Bartetko N., Hohoff C., Kuhl H., Franke R.,  
Boerchers T., Spener F.;  
RT "Mammary derived growth inhibitor is not a distinct protein but a mix  
of heart-type and adipocyte-type fatty acid-binding protein.";  
RL J. Biol. Chem. 271:19943-19949 (1996).  
CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG  
CHAIN FATTY ACID AND RETINOIC ACID (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF  
TRANSPORTER.  
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-----  
CC EMBL; X89244; CAA61532.1; -  
CC HSP; P04117; 1A2D.  
CC InterPro: IPR000463; Fatty acid BP.  
CC InterPro: IPR000566; Lipocalin; 1.  
CC Pfam; PF00061; lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.  
DR PROSITE; PS00214; FAMP; 1.  
KW Transport; Lipid-binding; Phosphorylation.  
FT INIT\_MET 0 BY SIMILARITY.  
FT MOD\_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)  
FT SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;  
Query Match 84.98; Score 573; DB 1; Length 131;  
Best Local Similarity 84.08; Pred. No. 1e-44;  
Matches 110; Conservative 8; Mismatches 13; Indels 0; Gaps 0;  
QY 2 CDAFVGWTKLVSSSENFDDYMEKVGFGFATRKVAGMAKPNLIISVNGDVITIKSESTFKNT 61  
DB 1 CDAFVGWTKLVSSSENFDDYMEKVGFGFATRKVAGMAKPNLIISVNGDVITIKSESTFKNT 60  
QY 62 EISFILGQEFDEVTDARRKVKSTITLGGVLVHVQKWDGKSTTKRKREDDKLVVECYMK 121  
DB 61 EISFKLGQEFDEITPDDRKVKSIIVLDBGALVQVQNDGKSTTKRKRLMDDKMLVECYMN 120  
QY 122 GVTSTRYVERA 132  
DB 121 GVTSTRYVERA 131  
RESULT 6  
MYP2\_RABIT  
ID MYP2\_RABIT STANDARD; PRT; 131 AA.  
AC P02691;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE MYELIN P2 PROTEIN.  
GN PMP2.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88228063; PubMed=2453513;  
RA Narayanan V., Barbosa E., Reed R., Tennekoon G.;  
RT "Characterization of a cloned cDNA encoding rabbit myelin P2  
protein.";  
RL J. Biol. Chem. 263:8332-8337 (1988).  
RN [2]  
RP SEQUENCE OF 1-55.  
RX MEDLINE=80094496; PubMed=7356651;  
RA Ishaque A., Hofmann T., Rhee S., Eylar E.H.;  
RT "The NH2-terminal region of the P2 protein from rabbit sciatic nerve  
myelin.";  
RL J. Biol. Chem. 255:1058-1063 (1980).  
RN [3]  
RP SEQUENCE OF 55-131.  
RX MEDLINE=82098098; PubMed=6172423;  
RA Ishaque A., Hofmann T., Eylar E.H.;  
RT "The complete amino acid sequence of the rabbit P2 protein.";  
RL J. Biol. Chem. 257:592-595 (1982).  
CC -1- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN  
CELLS.  
CC -1- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER  
CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN  
PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF  
TRANSPORTERS.  
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CC EMBL; X89244; CAA61532.1; -  
CC HSP; P04117; 1A2D.  
CC InterPro: IPR000463; Fatty acid BP.  
CC InterPro: IPR000566; Lipocalin; 1.  
CC Pfam; PF00061; lipocalin; 1.

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CC -----
DR EMBL; J03744; AAA31451.1;
DR PIR; A03145; MPRB2.
DR PIR; A28081; A28081.
DR HSP; P02690; LPMP.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocin_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT CONFLICT 72 72 E -> Q (IN REF. 3).
FT CONFLICT 83 83 I -> T (IN REF. 3).
FT CONFLICT 98 98 D -> N (IN REF. 3).
SQ SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRC64;
Query Match 71.4%; Score 482; DB 1; Length 131;
Best Local Similarity 72.4%; Pred. No. 1.5e-36;
Matches 92; Conservative 14; Mismatches 21; Indels 0; Gaps 0;
QY 5 FVGTWKLVSSENFDDYMKVEGVGFATRKVAGNAKPNMIIISVNGVDITIKSESTFKNTEIS 64
DB 4 FVGTWKLVSSENFDDYMKALGVGLATRLGNLAKPNVSIKSKGDIITITESTFKNTEIS 63
QY 65 FILGQEFFEVDATDKVAKSTITLDGVLVHVQKWDGKSTTIKKRREDDKLVVECVKMGVT 124
DB 64 FKLGEFEETADNKRKTSIIITLREGALNQVQKWDGKETTIRKLKLVQKGVVECKMGVV 123
QY 125 STRYVER 131
DB 124 CTRIYK 130
RESULT 7
FABP_RAT
ID FADH_RAT STANDARD; PRT; 132 AA.
DT 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FATTY ACID-BINDING PROTEIN, HEART (H-FABP).
GN FABP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67250640; PubMed=3036869;
RA Heckerth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
RT "Analysis of the tissue-specific expression, developmental
RT regulation, and linkage relationships of a rodent gene encoding heart
RT fatty acid binding protein.";
RL J. Biol. Chem. 262:9709-9717(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88107756; PubMed=3427112;
RA Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;
RT "Cloning and tissue distribution of rat heart fatty acid binding
RT protein mRNA: identical forms in heart and skeletal muscle.";
RL Biochemistry 26:7900-7904(1987).
RN [3]
RP SEQUENCE.
RX MEDLINE=88153733; PubMed=3162235;
RA Gibson B.W., Yu Z., Aberth W., Burlingame A.L., Bass N.M.;
RT "Revision of the blocked N terminus of rat heart fatty acid-binding
RT protein by liquid secondary ion mass spectrometry.";
RL J. Biol. Chem. 263:4182-4185(1988).
RN [4]

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RP PRELIMINARY SEQUENCE.
RX MEDLINE=86250713; PubMed=2424895;
RA Sacchetti J.C., Said B., Schulz H., Gordon J.I.;
RT "Rat heart fatty acid-binding protein is highly homologous to the
RT murine adipocyte 422 protein and the P2 protein of peripheral nerve
RT myelin.";
RL J. Biol. Chem. 261:8218-8223(1986).
RN [5]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=91170283; PubMed=2005132;
RA Kimura H., Odani S., Nishi S.-I., Sato H., Arakawa M., Ono T.;
RT "Primary structure and cellular distribution of two fatty
RT acid-binding proteins in adult rat kidneys.";
RL J. Biol. Chem. 266:5963-5972(1991).
RN [6]
RP SEQUENCE OF 58-86.
RX MEDLINE=89374061; PubMed=2775193;
RA Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;
RT "Rat heart fatty acid-binding protein. Evidence that supports the
RT amino acid sequence predicted from the cDNA.";
RL Biochem. J. 260:303-306(1989).
RN [7]
RP PARTIAL SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=90032682; PubMed=2806260;
RA Kanda T., Iseki S., Hitomi M., Kimura H., Odani S., Kondo H.,
RA Matsubara Y., Muto T., Ono T.;
RT "Purification and characterization of a fatty-acid-binding protein
RT from the gastric mucosa of rats. Possible identity with heart
RT fatty-acid-binding protein and its parietal cell localization.";
RL Eur. J. Biochem. 185:27-33(1989).
RN [8]
RP PARTIAL SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=88326235; PubMed=3415652;
RA Jones P.D., Carne A., Bass N.M., Grigor M.R.;
RT "Isolation and characterization of fatty acid binding proteins from
RT mammary tissue of lactating rats.";
RL Biochem. J. 251:919-925(1988).
RN [9]
RP PARTIAL SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=94162301; PubMed=8117746;
RA Nielsen S.U., Rump R., Roepstorff P., Spener F.;
RT "Differential regulation and phosphorylation of the fatty acid-
RT binding protein from rat mammary epithelial cells.";
RL Biochim. Biophys. Acta 1211:189-197(1994).
CC -1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: HEART, BUT ALSO SKELETAL MUSCLE, KIDNEY,
CC -1- BRAIN AND MAMMARY GLAND.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02773; AAA41136.1;
DR EMBL; M18034; AAA41137.1;
DR PIR; A23838; A23838.
DR PIR; A27452; A27452.
DR PIR; A28197; A28197.
DR PIR; A28458; A28458.
DR PIR; A39551; A39551.
DR PIR; S06478; S06478.
DR HSP; P05413; 2HMB.

```



"Isolation and sequence determination of cDNA encoding P2 protein of human peripheral myelin.";  
Biochem. Biophys. Res. Commun. 181:204-207(1991).  
[2]  
SEQUENCE.  
RX MEDLINE=83058785; PubMed=6183401;  
RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;  
RT "The complete amino acid sequence of human P2 protein.";  
RL J. Neurochem. 39:1759-1762(1982).  
[3]  
SEQUENCE OF 1-115 FROM N.A.  
RX MEDLINE=95054012; PubMed=7525873;  
RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,  
RA Tennekoon G.;  
RT "Partial structure and mapping of the human myelin P2 protein gene.";  
RL J. Neurochem. 63:2010-2013(1994).  
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.  
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF TRANSPORTERS.  
-----  
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EMBL; D16181; BAA03726.1; JOINED.  
EMBL; D16179; BAA03726.1; JOINED.  
EMBL; D16180; BAA03726.1; JOINED.  
EMBL; X62167; CAA44096.1; JOINED.  
EMBL; X73470; AAB32592.2; JOINED.  
EMBL; S73468; AAB32592.2; JOINED.  
EMBL; S73469; AAB32592.2; JOINED.  
PIR; A03143; MPB02.  
DR PIR; JT0977; JT0977.  
DR HSSP; P02690; 1PMP.  
DR MIW; 170715; -.  
DR InterPro; IPR000463; Fatty\_acid\_BP.  
DR InterPro; IPR000566; Lipocalin\_cytFABP.  
DR Pfam; PF00061; Lipocalin; 1.  
DR PRINTS; PR00178; FATTYACIDBP.  
DR PROSITE; PS00214; FAPB; 1.  
KW Myelin; Lipid-binding; Transport; Acetylation.  
FT INIT\_MET 0 0  
FT MOD\_RES 1 1 ACETYLYATION.  
FT DISULFID 117 124  
FT CONFLICT 24 24 G -> GG (IN REF. 3).  
FT CONFLICT 98 98 D -> N (IN REF. 2).  
FT CONFLICT 110 110 N -> D (IN REF. 2).  
SQ SEQUENCE 131 AA; 14778 MW; 300E640BA03E69D2 CRC64;  
  
Query Match 68.0%; Score 459; DB 1; Length 131;  
Best Local Similarity 68.5%; Pred. No. 1.7e-34;  
Matches 87; Conservative 16; Mismatches 24; Indels 0; Gaps 0;  
  
QY 5 FVGWTKLVSSNFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEIS 64  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 4 FLGTWTKLVSSNFDDYMKALGVGLATRLKGLNLAKEPRVLSKKGDIITIRTESTFKNTEIS 63  
  
QY 65 FILGQEFDEVTDARRKVKSTITLDGGVLVHVQKWDGKSTTTKRREDKLVVCEYKMGVT 124  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 64 FKLGOEFETADNRKTSVITLQSGSLNQVQWMDGKETTIRKLVKMGVAECKMGKV 123  
  
QY 125 STRVYER 131  
|:|||||:  
Db 124 CTRIYEK 130

RESULT 10  
MYP2\_BOVIN STANDARD; PRT; 131 AA.  
ID MYP2\_BOVIN STANDARD; PRT; 131 AA.  
AC P02690;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE MYELIN P2 PROTEIN.  
GN PMP2.  
OS Bos taurus (Bovine).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
CC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80225120; PubMed=6156092;  
RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;  
RT "The complete amino acid sequence of the P2 protein in bovine peripheral nerve myelin.";  
RL FEBS Lett. 115:27-30(1980).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
RX MEDLINE=89003045; PubMed=2458918;  
RA Jones T.A., Bergfors T., Sedzik J., Unge T.;  
RT "The three-dimensional structure of P2 myelin protein.";  
RL EMBO J. 7:1597-1604(1988).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
RX MEDLINE=93253782; PubMed=7683727;  
RA Cowan S.W., Newcomer M.E., Jones T.A.;  
RT "Crystallographic studies on a family of cellular lipophilic transport proteins. Refinement of P2 myelin protein and the structure determination and refinement of cellular retinol-binding protein in complex with all-trans-retinol.";  
RL J. Mol. Biol. 230:1225-1246(1993).  
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.  
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF TRANSPORTERS.  
CC PIR; A03144; MPB02.  
DR PDB; 1PMP; 26-JAN-95.  
DR InterPro; IPR000463; Fatty\_acid\_BP.  
DR InterPro; IPR000566; Lipocalin\_cytFABP.  
DR Pfam; PF00061; Lipocalin; 1.  
DR PRINTS; PR00178; FATTYACIDBP.  
DR PROSITE; PS00214; FAPB; 1.  
KW Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.  
FT MOD\_RES 1 1 ACETYLYATION.  
FT DISULFID 117 124  
SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;  
  
Query Match 66.4%; Score 448; DB 1; Length 131;  
Best Local Similarity 67.7%; Pred. No. 1.6e-33;  
Matches 86; Conservative 16; Mismatches 25; Indels 0; Gaps 0;  
  
QY 5 FVGWTKLVSSNFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEIS 64  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 4 FLGTWTKLVSSNFDDYMKALGVGLATRLKGLNLAKEPRVLSKKGDIITIRTESTFKNTEIS 63  
  
QY 65 FILGQEFDEVTDARRKVKSTITLDGGVLVHVQKWDGKSTTTKRREDKLVVCEYKMGVT 124  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 64 FKLGOEFETADNRKTSVITLQSGSLNQVQWMDGKETTIRKLVKMGVAECKMGKV 123  
  
QY 125 STRVYER 131  
|:|||||:  
Db 124 CTRIYEK 130

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RESULT 11
MYP2_MOUSE STANDARD; PRT; 131 AA.
ID MYP2_MOUSE AC P24526;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYELIN P2 PROTEIN.
GN PMP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268811; PubMed=1711100;
RA Narayanan V., Kaestner K.H., Tennekoon G.I.;
RT "Structure of the mouse myelin P2 protein gene.";
RL J. Neurochem. 57:75-80(1991).
CC -1- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -1- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S39508; AAB19249.2;
DR PIR; JH0407; JH0407.
DR HSP; P02690; PMP2.
DR MGD; MGI:102667; Pmp2.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
DR Myelin; Lipid-binding; Transport; Acetylation.
KW MYELIN; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14804 MW; AB357746F152E07C CRC64;

Query Match 66.1%; Score 446; DB 1; Length 131;
Best Local Similarity 66.1%; Pred. No. 2.5e-33;
Matches 84; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 5 FVGTWKLVSSENFDDYKVEGVGATRKVACMAKPNMIISVNGDVITIKSESTFKNTEIS 64
Db 4 FLGTWKLVSSEHFDYMKALGVGLANRLAKPTVITISKKDYITITRTSFAFKNTEIS 63
QY 65 FILGQFDEVTADRRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDKLVVECVKMGVT 124
Db 64 FKLGQFDEVTADNRKAKSIYTLERGLSKVQKWDGKETAIRTLILDRGVVVEICMGV 123
QY 125 STRYIER 131
Db 124 CTRIYK 130

RESULT 12
FABH_HUMAN STANDARD; PRT; 132 AA.
ID FABH_HUMAN AC P05413; Q99957;

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DT 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FATTY ACID-BINDING PROTEIN, HEART (H-FABP) (MUSCLE FATTY ACID-BINDING
DE PROTEIN) (M-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDGI).
GN FABP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RX MEDLINE=91248148; PubMed=1710107;
RA Peeter R.A., Veerkamp J.H., Kanda T., Ono T., Geurts van Kessel A.;
RT "Cloning of the cDNA encoding human skeletal-muscle
RT fatty-acid-binding protein, its peptide sequence and chromosomal
RT localization.";
RL Biochem. J. 276:203-207(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Breast;
RA Hu Y.F., Ao X., Russo I.H., Russo J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wu X., Arlt M., Goodfellow P.J., Rottman J.N.;
RT "Genomic organization and complete nucleotide sequence of the human
RT cardiac fatty acid binding protein gene (FABP3), and identification of
RT a closely related genomic sequence.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE.
RX MEDLINE=88339792; PubMed=3421901;
RA Offner G.D., Brecher P., Sawilovich W.B., Costello C.E., Troxler R.F.;
RT "Characterization and amino acid sequence of a fatty acid-binding
RT protein from human heart.";
RL Biochem. J. 252:191-198(1988).
RN [5]
RP REVISIONS, AND SEQUENCE.
RX MEDLINE=91094793; PubMed=2266954;
RA Boerchers T., Hoejrup P., Nielsen S.U., Roepstorff P., Spener F.,
RA Knudsen J.;
RT "Revision of the amino acid sequence of human heart fatty
RT acid-binding protein.";
RL Mol. Cell. Biochem. 98:127-133(1990).
RN [6]
RP SEQUENCE OF 14-132 FROM N.A.
RX TISSUE=Heart;
RX MEDLINE=94085953; PubMed=8262516;
RA Troxler R.F., Offner G.D., Jiang J.W., Wu B.L., Skare J.C.,
RA Milunsky A., Wyandt H.E.;
RT "Localization of the gene for human heart fatty acid binding protein
RT to chromosome 1p32-1p33.";
RL Hum. Genet. 92:563-566(1993).
RN [7]
RP SEQUENCE OF 31-38.
RX TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyamov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=92406763; PubMed=1526991;
RA Zanotti G., Scapin G., Spadon P., Veerkamp J.H., Sacchettini J.C.;
RT "Three-dimensional structure of recombinant human muscle fatty acid-
RT binding protein.";
RL J. Biol. Chem. 267:18541-18550(1992).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).

```





RT "Purification and characterisation of a polymorphic low M(r) bovine  
RT muscle cysteine proteinase inhibitor: structural identity with fatty-  
RT acid-binding proteins.";  
RL Biochimie 75:937-945(1993).

[6]

RN VARIANT IN POSITION 98.  
RP MEDLINE-93358876; PubMed-8354262;  
RX Bartetzko N., Lezius A.G., Spener F.;  
RA "Isoforms of fatty-acid-binding protein in bovine heart are coded by  
RT distinct mRNA";  
RL Eur. J. Biochem. 215:555-559(1993).

[7]

RN X-RAY CRYSTALLOGRAPHY.  
RP MEDLINE-91301134; PubMed-2070787;  
RX Mueller-Fahnow A., Egner U., Jones T.A., Ruedel H., Spener F.,  
RA Saenger W.;  
RT "Three-dimensional structure of fatty-acid-binding protein from  
RL bovine heart";  
RL Eur. J. Biochem. 199:271-276(1991).

[8]

RN STRUCTURE BY NMR.  
RP MEDLINE-93130916; PubMed-1483473;  
RX Luecke C., Lassen D., Krelenkamp H.-J., Spener F., Rueterjans H.;  
RA "Sequence-specific 1H-NMR assignment and determination of the  
RT secondary structure of bovine heart fatty-acid-binding protein";  
RL Eur. J. Biochem. 210:901-910(1992).

[9]

RN STRUCTURE BY NMR.  
RP MEDLINE-95324534; PubMed-7601110;  
RX Lassen D., Luecke C., Kveder M., Mesgarzadeh A., Schmidt J.M.,  
RA Specht B., Lezius A., Spener F., Rueterjans H.;  
RT "Three-dimensional structure of bovine heart fatty-acid-binding  
RL protein with bound palmitic acid, determined by multidimensional NMR  
spectroscopy";  
RL Eur. J. Biochem. 230:266-280(1995).

[10]

RN STRUCTURE BY NMR.  
RP MEDLINE-98149696; PubMed-9490052;  
RX Mesgarzadeh A., Pfeiffer S., Engelke J., Lassen D., Rueterjans H.;  
RA "Bound water in apo and holo bovine heart fatty-acid-binding protein  
RT determined by heteronuclear NMR spectroscopy";  
RL Eur. J. Biochem. 251:781-786(1998).

[11]

CC -1- FUNCTION: FAPP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR  
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -1- FUNCTION: MGI REVERSIBLY INHIBITS PROLIFERATION OF MAMMARY

CC CARCINOMA CELLS.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC OR MITOCHONDRIAL MATRIX.

CC -1- TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELLS OF DEVELOPING

CC LOBULOALVEOLAR STRUCTURES AND HEART.

CC -1- SIMILARITY: BELONGS TO THE FAPP/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; X12710; CAA31212.1; -

CC EMBL; X51933; CAA36199.1; -

CC PIR; A29466; A29466.

CC PIR; S01133; S01133.

CC PIR; A34676; A34676.

CC PIR; A37883; A37883.

CC PDB; 1BWY; 07-OCT-98.

CC InterPro; IPR000463; Fatty\_acid\_BP.

CC InterPro; IPR000566; Lipocin\_cytFAPP.

CC Pfam; PF00061; lipocalin; 1.

CC PRINTS; PR00178; FATTYACIDBP.

CC PROSITE; PS00214; FAPP; 1.

CC Transport; Lipid-binding; Acetylation; Phosphorylation; 3D-structure.

CC -----

FT INIT\_MET 0 0  
FT MOD\_RES 1 1 ACETYLATION.  
FT MOD\_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)  
FT MOD\_RES 19 19 (BY SIMILARITY).  
FT VARIANT 98 98 N -> D.  
FT CONFLICT 12 14 DSK -> SSE (IN REF. 4).  
FT CONFLICT 40 40 T -> L (IN REF. 4).  
FT CONFLICT 43 43 E -> S (IN REF. 4).  
FT CONFLICT 93 93 H -> Q (IN REF. 4).  
FT CONFLICT 127 127 T -> V (IN REF. 4).  
FT SEQUENCE 132 AA; 14648 MW; C6204932C6DFD35 CRC64;

Query Match 65.58; Score 442; DB 1; Length 132;  
Best Local Similarity 65.18; Pred. No. 5.7e-33;  
Matches 84; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

QY 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPMNLIISVNGDVITIKSETFKNT 62  
Db 2 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPMNLIISVNGDVITIKSETFKNT 61

QY 63 ISFILGQEFDEVTADRRKVKSTITLDGGLVHVQKWDGKSTTKRKREDDKLWECVMKG 122  
Db 62 ISFVLGVFEFDEVTADRRKVKSTITLDGGLVHVQKWDGKSTTKRKREDDKLWECVMKG 121

QY 123 VTSTRVYER 131  
Db 122 AVCTRTYEK 130

#### RESULT 14

ID FABH\_PIG STANDARD; PRT; 132 AA.  
AC 002772;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE FATTY ACID-BINDING PROTEIN, HEART (H-FAPP).  
OS FAPP3.  
GN Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE-97262098; PubMed-9107676;  
RA Gerbens F.N.A., Rottenberger G., Lenstra J.A., Veerkamp J.H.,  
RA Te Pas M.F.W.;  
RT "Characterization, chromosomal localization, and genetic variation of  
RL the porcine heart fatty acid-binding protein gene";  
RL Mann. Genome 8:328-332(1997).  
CC -1- FUNCTION: FAPP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR  
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
CC -1- SIMILARITY: BELONGS TO THE FAPP/P2/CRBP/CRABP FAMILY OF  
CC TRANSPORTERS.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL; X98558; CAA67168.1; -

CC HSPB; P10790; 1BWY.

CC InterPro; IPR000463; Fatty\_acid\_BP.

CC InterPro; IPR000566; lipocin\_cytFAPP.

CC Pfam; PF00061; lipocalin; 1.

CC PRINTS; PR00178; FATTYACIDBP.

CC PROSITE; PS00214; FAPP; 1.

CC -----

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KW Transport; Lipid-binding; Acetylation; Phosphorylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES) (BY
FT SIMILARITY).
SQ SEQUENCE 132 AA; 14618 MW; B5431B652F596C95 CRC64;

Query Match 65.5%; Score 442; DB 1; Length 132;
Best Local Similarity 65.1%; Pred. No. 5.7e-33;
Matches 84; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
Db 2 DAFAGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61
Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKDGKSTTIKKREDDDKLVECVKMG 122
Db 62 ISFGLGVEFDEVTADDRKVKSTITLDGGVLHVQKDGKSTTIKKREDDDKLVECVKMG 122
Qy 123 VTSTRVYER 131
Db 122 AVCTRTYER 130

RESULT 15
FABB_BOVIN
ID FABB_BOVIN STANDARD; PRT; 131 AA.
AC Q09139;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FATTY ACID-BINDING PROTEIN, BRAIN (B-FABP).
GN FABP7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91094811; PubMed=2266968;
RA Schoentgen F., Bonanno L.M., Pignede G., Jolles P.;
RT "Amino acid sequence and some ligand binding properties of fatty
FT acid-binding protein from bovine brain.";
RL Mol. Cell. Biochem. 98:35-39(1990).
RN [2]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90032683; PubMed=2806261;
RA Schoentgen F., Pignede G., Bonanno L.M., Jolles P.;
RT "Fatty-acid-binding protein from bovine brain. Amino acid sequence
FT and some properties.";
RL Eur. J. Biochem. 185:35-40(1989).
CC -1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC BINDS OLEIC AND PALMITIC ACIDS BUT NOT PALMITOYL COA.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
KW Transport; Lipid-binding.
FT VARIANT 11 12 TE -> VD.
FT VARIANT 14 14 Q -> K.
FT VARIANT 18 18 E -> D.
FT VARIANT 33 34 GN -> AS.
FT VARIANT 40 40 L -> T.

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FT VARIANT 43 44 SV -> EK.
FT VARIANT 49 49 E -> V.
FT VARIANT 65 65 H -> K.
FT VARIANT 68 68 E -> V.
FT VARIANT 72 72 D -> E.
FT VARIANT 78 78 Q -> R.
FT VARIANT 83 83 I -> V.
FT VARIANT 105 105 V -> T.
FT VARIANT 108 108 M -> L.
FT VARIANT 121 122 DV -> TA.
FT VARIANT 127 127 H -> T.
SQ SEQUENCE 131 AA; 14590 MW; A26FF5D63C0CF2B4 CRC64;

Query Match 63.0%; Score 425; DB 1; Length 131;
Best Local Similarity 62.0%; Pred. No. 1.9e-31;
Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
Db 2 DAFVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61
Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKDGKSTTIKKREDDDKLVECVKMG 122
Db 62 ISFHLGEEFDDTADDRKVKSTITLDGGVLHVQKDGKSTTIKKREDDDKLVECVKMG 121
Qy 123 VTSTRVYER 131
Db 122 VVAVRHYEK 130

Search completed: January 24, 2002, 09:18:21
Job time: 178 sec

```

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 09:15:43 ; Search time 25.01 Seconds  
(without alignments)  
772.009 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MCDAFVGTWKLVSSENFDDY.....KLVVECVMGVSTRVYERA 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

SPTREMBL\_17:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.invertebrate:\*  
14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	96.4	132	11 Q99P60	Q99P60 spermophilu
2	603	89.3	150	11 Q9R290	Q9R290 rattus norv
3	537	79.6	113	6 Q9XSG4	Q9XSG4 oryctolagus
4	473.5	70.1	134	11 Q9QY04	Q9QY04 rattus norv
5	468	69.3	133	11 Q99P61	Q99P61 spermophilu
6	433	64.1	99	6 Q97675	Q97675 sus scrofa
7	427	63.3	125	6 Q9XSI5	Q9XSI5 equus caball
8	413	61.2	132	13 Q918N9	Q918N9 brachydanio
9	402	59.6	132	11 Q9DAL2	Q9DAL2 mus musculu
10	400	59.3	133	13 Q57668	Q57668 cryodrac a
11	397	58.8	133	13 Q57667	Q57667 chaenoceph
12	397	58.8	133	13 Q57670	Q57670 gobionototh
13	393.5	58.3	134	13 Q57691	Q57691 cryodrac a
14	392	58.1	133	13 Q57669	Q57669 nototheria
15	391.5	58.0	134	13 Q57666	Q57666 paracheaen
16	390.5	57.9	134	13 Q57665	Q57665 gobionototh
17	387.5	57.4	134	13 Q57663	Q57663 nototheria
18	384	56.9	135	13 Q91896	Q91896 anguilla ja
19	379	56.1	166	4 Q9H047	Q9H047 homo sapien

20	374	55.4	132	11 Q9DAK4	Q9DAK4 mus musculu
21	341	50.5	97	11 Q9QV90	Q9QV90 mus sp. lmg
22	307.5	45.6	135	5 Q01812	Q01812 caenorhabdi
23	300.5	44.5	136	5 Q01814	Q01814 caenorhabdi
24	285	42.2	130	5 Q9VGM2	Q9VGM2 drosophila
25	270.5	40.1	133	5 Q9BMK1	Q9BMK1 echinococcu
26	270.5	40.1	133	5 Q9BLY5	Q9BLY5 echinococcu
27	256.5	38.0	137	5 Q02323	Q02323 caenorhabdi
28	254.5	37.7	132	5 Q026517	Q026517 schistosoma
29	252	37.3	132	5 Q61236	Q61236 manduca sex
30	248.5	36.8	133	5 Q9BMK2	Q9BMK2 echinococcu
31	247.5	36.7	100	13 Q57664	Q57664 rhigophila
32	247.5	36.2	132	5 Q9BME8	Q9BME8 schistosoma
33	244.5	36.2	133	5 Q9BMK3	Q9BMK3 echinococcu
34	231.5	34.3	132	5 Q45035	Q45035 schistosoma
35	224	33.2	134	11 Q9EPC5	Q9EPC5 mus musculu
36	222	32.9	134	11 Q9DIN1	Q9DIN1 mus musculu
37	210	31.1	114	11 Q99M00	Q99M00 mus musculu
38	204.5	30.3	120	5 Q45036	Q45036 schistosoma
39	201.5	29.9	132	5 Q9ULG6	Q9ULG6 fasciola he
40	189.5	28.1	147	13 Q9PSA5	Q9PSA5 xenopus lae
41	184	27.3	132	13 Q9PRH9	Q9PRH9 brachydanio
42	167	24.7	176	5 Q02324	Q02324 caenorhabdi
43	165	24.4	135	4 P82980	P82980 homo sapien
44	157.5	23.3	126	13 Q918L5	Q918L5 brachydanio
45	156.5	23.2	132	5 Q9UAS2	Q9UAS2 fasciola gi

#### ALIGNMENTS

#### RESULT 1

Q99P60 PRELIMINARY; PRT; 132 AA.  
AC Q99P60  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ADIPOSE-TYPE FATTY ACID-BINDING PROTEIN.  
GN FABP4.  
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scluridae; Sclurinae;  
OC Spermophilus.  
OX NCBI\_TaxID=43179;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hittell D.S., Storey K.B.;  
RT "Differential expression of adipose- and heart-type fatty acid-binding proteins in hibernating ground squirrels."  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF327855; AAK08084.1; .  
SQ SEQUENCE 132 AA; 14765 MW; FCBI4230E34C0708 CRC64;

Query Match 96.4%; Score 651; DB 11; Length 132;  
Best Local Similarity 97.0%; Pred. No. 5.1e-50;  
Matches 128; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVEGVGFATRKVAGAKPMNIISVNGDVITIKSESTFKN 60

DB 1 MCDAFVGTWKLVSSENFDDYMKVEGVGFATRKVAGAKPMNIISVNGDVITIKSESTFKN 60

QY 61 TETSFILGQEFDEVTADDRKVKSTIILDGVLVHVQKWDGKSTTIKKRDEDDKLWVECVN 120

DB 61 TETSFILGQEFDEVTADDRKVKSTIILDGVLVHVQKWDGKSTTIKKRDEDDKLWVECVN 120

QY 121 KGVTSRTRYERA 132

DB 121 KGVTSRTRYERA 132

#### RESULT 2

```
Q9R290
ID Q9R290 PRELIMINARY; PRT; 150 AA.
AC Q9R290;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ADIPOCYTE LIPID-BINDING PROTEIN.
GN ALBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=ADIPOSE TISSUE;
RX MEDLINE=99254074; PubMed=10318917;
RA Shen W.-J., Sridhar K., Bernlohr D.A., Kraemer F.B.;
RT "Interaction of rat hormone-sensitive lipase with adipocyte lipid-
binding protein."
RL Proc. Natl. Acad. Sci. U.S.A. 96:5528-5532(1999).
DR EMBL; AF144756; AAD37371.1; -.
DR HSP; P04117; ILLD.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 150 AA; 16468 MW; 9D214AB610D0C54E CRC64;

Query Match 89.3%; Score 603; DB 11; Length 150;
Best Local Similarity 87.9%; Pred. No. 9.9e-46;
Matches 116; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKN 60
Db 1 MCDAPVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNLIISVEGDLVIRSESTFKN 60

QY 61 TEISFILGQEFDEVTAADRKVKSITLDGGVLHVQKWDGKSTIKRKREDDKLVEECVM 120
Db 61 TEISFKLGVEFEITPDPRKVKSIITLDGGVLHVQKWDGKSTIKRKXDGDKLVEECVM 120

QY 121 KGVSTRVYERA 132
Db 121 KGVSTRVYXRA 132

RESULT 3
Q9XSG4
ID Q9XSG4 PRELIMINARY; PRT; 113 AA.
AC Q9XSG4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ADIPOCYTE LIPID-BINDING PROTEIN (FRAGMENT).
GN AP2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=BLADDER;
RA Guan Y., Zhang Y., Davis L., Breyer M.D.;
RT "Expression of ap2 gene in transitional epithelium of rabbit
bladder."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF136241; AAD32209.1; -.
DR HSP; P04117; ILLD.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
```

```
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12536 MW; 4C19A538EC897F4F CRC64;

Query Match 79.6%; Score 537; DB 6; Length 113;
Best Local Similarity 94.7%; Pred. No. 4.4e-40;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 8 TWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKNTEISFIL 67
Db 1 TWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKNTEISFKL 60

QY 68 GQEFDEVTAADRKVKSIITLDGGVLHVQKWDGKSTIKRKREDDKLVEECVM 120
Db 61 GQEFDEVTAADRKVKSIITLDGGALVQVQKWDGKSTIKRKREGDKLVEECVM 113

RESULT 4
Q9QY04
ID Q9QY04 PRELIMINARY; PRT; 134 AA.
AC Q9QY04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FATTY ACID-BINDING PROTEIN.
GN FABP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=HEART;
RX PubMed=10561574;
RA Zhang J., Rickers-Haunerland J., Dawe I., Haunerland N.H.;
RT "Structure and chromosomal location of the rat gene encoding the heart
fatty acid-binding protein."
RL Eur. J. Biochem. 266:347-351(1999).
DR EMBL; AF144090; AAF19003.1; -.
DR HSP; P05413; IHMT.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 14888 MW; BE87C12F10992FF4 CRC64;

Query Match 70.1%; Score 473.5; DB 11; Length 134;
Best Local Similarity 70.5%; Pred. No. 2.1e-34;
Matches 93; Conservative 12; Mismatches 26; Indels 1; Gaps 1;

QY 1 MCDAPVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKN 60
Db 1 MADAPVGTWKLVDKSNFDDYKMSLGVGFGFATRKQVASMTKPTTIIKNGDITTIKTHSTFKN 60

QY 61 TEISFILGQEFDEVTAADRKVKSITLDGGVLHVQKWDGKSTIKRKREDDKLVEECVM 120
Db 61 TEISFQLGVEFEDEVTAADRKVKSIVTLDGGKLHVQKWDGQETTLTRELSDGKLILTLT 120

QY 121 KG-VTSTRVYER 131
Db 121 HGVVSTRVYER 132

RESULT 5
Q99P61
ID Q99P61 PRELIMINARY; PRT; 133 AA.
AC Q99P61;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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RESULT 7
Q9XS15
ID Q9XS15 PRELIMINARY; PRT; 125 AA.
AC Q9XS15;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HEART-TYPE FATTY ACID-BINDING PROTEIN (FRAGMENT).
GN FAPB3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Schaaap F.G., Pellers M.M.A.L., Van der Vusse G.J., Glatz J.F.C.;
RT "Cloning of equine H-FABP cDNA.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF143950; AAD32219.1; -
DR HSSP; P10750; 1BWY
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
FT NON_TER 1
SQ SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;

Query Match 63.3%; Score 427; DB 6; Length 125;
Best Local Similarity 66.7%; Pred. No. 2.3e-30;
Matches 82; Conservative 13; Mismatches 28; Indels 0; Gaps

QY 9 WKLVSSSEDDYMKVGVGFATRKVAGMAKPMIISVNGDVITIKSESTFKNTEISFILG 68
DB 1 WKLVSKNFDDYMKVSGVGFATRVQANNTKPTTIEVNGDITITKHTSEKTEISFKLG 60
QY 69 QEFDEVTADRRKVKSTITLDGVLVHVOKDGKSTIKRKREDDKLVVCEVMKGVSTRV 128
DB 61 VEDETTADRRKVKSLVDLGGKLVHVQEWNGQETTLVRELIDGKLTLTHGSASVSTRT 120
QY 129 YET 131
DB 121 YEK 123

RESULT 8
Q9I8N9
ID Q9I8N9 PRELIMINARY; PRT; 132 AA.
AC Q9I8N9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BRAIN-TYPE FATTY-ACID BINDING PROTEIN.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Denovan-Wright E.M., Pierce M., Wright J.M.;
RT "Nucleotide sequence of cDNA clones coding for a brain-type fatty acid
binding protein and its tissue-specific expression in adult zebrafish
(Danio rerio).";
RL Biochim. Biophys. Acta 0:0-0(2000).
DR EMBL; AF237712; AAF79948.1; -
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.

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DR PROSITE; PS00214; FARP; 1.
SQ SEQUENCE 132 AA; 14918 MW; ED59506C71994C55 CRC64;

Query Match
Best Local Similarity 61.2%; Score 413; DB 13; Length 132;
Matches 78; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MVDFACTATKLVDSQNFDEYMKSLGVGFATRVQGNVTKPTIVISHEGDKVVIKLSFTKN 60

QY 61 TEISFILGQEFDEVTAADRRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TEISFKLGEFEETADNRKVKSLITFEGGSMIQVQKWLKGKQTTIKRKIVDKKVVECTM 120

QY 121 KGVSTRYER 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 EGVQAVRYERA 132

RESULT 9
Q9DAL2 PRELIMINARY; PRT; 132 AA.
AC Q9DAL2:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1700007P10RIK PROTEIN.
GN 1700007P10RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyoko-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005745; BAB24218.1; -.
DR MGD; MGI:1917230; 1700007P10RIK.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FARP; 1.
SQ SEQUENCE 132 AA; 15017 MW; D52B2279F0A7E272 CRC64;

Query Match
Best Local Similarity 59.6%; Score 402; DB 11; Length 132;
Matches 77; Conservative 24; Mismatches 30; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
```

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Db 1 MIEPFLGTWKLVSSENFENFVRELGVCEPRKVKACLKPSVISFNGERMDIQGSACRN 60

QY 61 TEISFILGQEFDEVTAADRRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TEISFKLGEFEETADNRKVKSLITFEGGSMIQVQKWLKGKQTTIKRKIVDKKVVECTM 120

QY 121 KGVSTRYER 131
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 NNVSRIYER 131

RESULT 10
O57668 PRELIMINARY; PRT; 133 AA.
AC O57668:
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FATTY ACID BINDING PROTEIN H8-ISOFORM.
GN H8-FABP.
OS Cryodraco antarcticus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidei; Channichthyidae; Cryodraco.
OX NCBI_TaxID=36192;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;

RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RT heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92449; AAC60357.1; -.
DR HSP; P10790; IBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
SQ SEQUENCE 133 AA; 15011 MW; 1E691AA2738C75FF CRC64;

Query Match
Best Local Similarity 59.3%; Score 400; DB 13; Length 133;
Matches 77; Conservative 18; Mismatches 37; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MVDVFGTWNKLDSEKDEYMKSLGVGFATRVQGNVTKPTIISVEGDKVILKTSQAIKN 60

QY 61 TEISFILGQEFDEVTAADRRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TEISFKLDEEDETADRRKVKSVFTLDGGLVHTQKWDGKSTSLVREVNGNSLTLLKM 120

QY 121 KGVSTRYER 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 DDVESIRRYKA 132

RESULT 11
O57667 PRELIMINARY; PRT; 133 AA.
AC O57667:
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FATTY ACID BINDING PROTEIN H8-ISOFORM.
GN H8-FABP.
OS Chaenocoepalus aceratus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
 OC Notothenioidei; Channichthyidae; Chaenoccephalus.  
 OX NCBI\_TaxID=36190;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART VENTRICLE;

RX MEDLINE=98129752; PubMed=9461533;

RA Vayda M.E., Londraville R.L., Cashion R.E., Costello L., Sidell B.D.;

RT "Two distinct types of fatty acid-binding protein are expressed in

heart ventricle of Antarctic teleost fishes.";

RL Biochem. J. 330:375-382(1998).

DR EMBL; U92448; AAC60356.1; -

DR HSSP; P10790; IBWY.

DR InterPro; IPR000463; Fatty\_acid\_BP.

DR InterPro; IPR000566; Lipocln\_cytfabp.

DR Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.

SQ SEQUENCE 133 AA; 15024 MW; 85157AA2665658C3 CRC64;

Query Match 58.8%; Score 397; DB 13; Length 133;

Best Local Similarity 57.6%; Pred. No. 1.1e-27;

Matches 76; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

OY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

DB 1 MVDVFGTWNKDKSEKDEYMKKLGVGATRQGVNVTPTTIISVEGDKVTLKQSAIKN 60

OY 61 TEISFILGOEFDETTADDRKVKSTITLDGGVLHVQKWDGKSTTKRKRDEDDKLVEECVM 120

DB 61 TELSFKLDEFEDETTADDRKVKSEFTVDGGKLVHTQKWDGKSTSLVREVNGNSLTLTKM 120

OY 121 KGVSTRVYERA 132

DB 121 DDVESIRRYVKA 132

RESULT 12

OY 057670 PRELIMINARY; PRT; 133 AA.

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE FATTY ACID BINDING PROTEIN H8-ISOFORM.

GN H8-FABP.

OS Gobionotothen gibberifrons.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

OC Notothenioidei; Nototheniidae; Gobionotothen.

OX NCBI\_TaxID=36202;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART VENTRICLE;

RX MEDLINE=98129752; PubMed=9461533;

RA Vayda M.E., Londraville R.L., Cashion R.E., Costello L., Sidell B.D.;

RT "Two distinct types of fatty acid-binding protein are expressed in

heart ventricle of Antarctic teleost fishes.";

RL Biochem. J. 330:375-382(1998).

DR EMBL; U92451; AAC60359.1; -

DR HSSP; P10790; IBWY.

DR InterPro; IPR000463; Fatty\_acid\_BP.

DR InterPro; IPR000566; Lipocln\_cytfabp.

DR Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.

SQ SEQUENCE 133 AA; 14997 MW; 85157AA2738C68C3 CRC64;

Query Match

Best Local Similarity

Matches

76; Conservative

19; Mismatches

37; Indels

0; Gaps

0;

OY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

DB 1 MVDVFGTWNKDKSEKDEYMKKLGVGATRQGVNVTPTTIISVEGDKVTLKQSAIKN 60

OY 61 TEISFILGOEFDETTADDRKVKSTITLDGGVLHVQKWDGKSTTKRKRDEDDKLVEECVM 120

DB 61 TELSFKLDEFEDETTADDRKVKSEFTVDGGKLVHTQKWDGKSTSLVREVNGNSLTLTKM 120

OY 121 KGVSTRVYERA 132

DB 121 DDVESIRRYVKA 132

RESULT 13

OY 057691 PRELIMINARY; PRT; 134 AA.

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE FATTY ACID BINDING PROTEIN H6-ISOFORM.

GN H6-FABP.

OS Cryodraco antarcticus, and

OC Chaenoccephalus aceratus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

OC Notothenioidei; Channichthyidae; Cryodraco.

OX NCBI\_TaxID=36192; 36190;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART VENTRICLE;

RA Vayda M.E., Londraville R.L., Cashion R.E., Costello L., Winnard P.,

RA Small D.J., Hatch H., Sidell B.D.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; U92443; AAC60351.1; -

DR HSSP; U92442; AAC60350.1; -

DR InterPro; IPR000463; Fatty\_acid\_BP.

DR InterPro; IPR000566; Lipocln\_cytfabp.

DR Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.

DR PROSITE; PS00214; FABP; 1.

SQ SEQUENCE 134 AA; 15138 MW; D4CBFC689147A98 CRC64;

Query Match 58.3%; Score 393.5; DB 13; Length 134;

Best Local Similarity 55.4%; Pred. No. 2.2e-27;

Matches 72; Conservative 23; Mismatches 34; Indels 1; Gaps 1;

OY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 59

DB 1 MVEKFGVTWKLVISSDNFDDYMKVGVGFATRQGVNVTPTTIISVEGDKVTLKQSAIKN 60

OY 60 NTEISFILGOEFDETTADDRKVKSTITLDGGVLHVQKWDGKSTTKRKRDEDDKLVEECV 119

DB 61 TTEIKFLNPFETTTADDRKTKTVVTVLENGKLVQKQSWDGKSTNIEIEDGKLVAKCI 120

OY 120 MKGVSTRVY 129

DB 121 MGDVIAVRTY 130

RESULT 14

OY 057669 PRELIMINARY; PRT; 133 AA.

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE FATTY ACID BINDING PROTEIN H8-ISOFORM.

GN H8-FABP.

OS Notothenia coriiceps neglecta (Black rockcod) (Yellowbelly rockcod).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Notothenia.
OX NCBI_TaxID=8209;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RL heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92450; AAC60358.1; -.
DR HSSP; P10790; IBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
SQ SEQUENCE 133 AA; 15008 MW; 851B94538D6E78DE CRC64;

Query Match 58.1%; Score 392; DB 13; Length 133;
Best Local Similarity 56.8%; Pred. No. 3e-27;
Matches 75; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGD-VITIKSESTFK 60
DB 1 MVDVFGVIWNLKDEKDEYMKLVGVGFATRKVGNVTKPTIISVEGDKVTLKTQSAIKN 60
QY 61 TEISFILGOEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKRKREDDKLVVECV 120
DB 61 TELSKLNEEFDEFTADDRKVKSPVTVDGKLVHVKQKWDGKSTTIKRKREDDKLVVECV 120
QY 121 KGVSTRYERA 132
DB 121 DDVESIRRYVKA 132

RESULT 15
O57666 PRELIMINARY; PRT; 134 AA.
AC O57666;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FATTY ACID BINDING PROTEIN H6-ISOFORM.
GN H6-FABP.
OS Parachaenichthys charcoti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Bathyracidae; Parachaenichthys.
OX NCBI_TaxID=36187;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RL heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92447; AAC60355.1; -.
DR HSSP; P10790; IBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15161 MW; D4CBFC689121AFE CRC64;
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Query Match 58.0%; Score 391.5; DB 13; Length 134;

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Best Local Similarity 55.4%; Pred. No. 3.4e-27;
Matches 72; Conservative 23; Mismatches 34; Indels 1; Gaps 1;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGD-VITIKSESTFK 59
DB 1 MVEKFGVTWKNMISDNFDDYMKVGVGFATRKVGNVTKPNLVSVDDQGFVCLKSQSTFK 60
QY 60 NTEISFILGOEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKRKREDDKLVVECV 119
DB 61 TTEIKFKLNEPFETTTADDRKTKVTVTLENGKLVQKQSDGKETHIERIEDGKLVAKCI 120
QY 120 MKGVSTRVY 129
DB 121 MGDVIAVRTY 130

Search completed: January 24, 2002, 09:18:54
Job time: 191 sec
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